

Scoring table:	BLOSUM62
Title:	US-10-612-885A-1
Perfect score:	117
Sequence:	1 QRVEILEGRTECVLSNLGRTRRY 23
Run on:	May 6, 2004, 12:41:36 ; Search time 39 Seconds (without alignments) 186.075 Million cell updates/sec
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	SPTRNBL_25: 1: SP_arChaea: * 2: SP_bacteria: * 3: .SP_fungi: * 4: SP_human: * 5: SP_invertebrate: * 6: SP_mammal: * 7: SP_mhc: * 8: SP_organelle: * 9: SP_Phage: * 10: SP_plant: * 11: SP_rRodent: * 12: SP_virus: * 13: SP_vertebrate: * 14: SP_unclassified: * 15: SP_rvirus: * 16: SP_bacteria: * 17: SP_archeap: *

## ALIGNMENTS

Score	Query	Match	Length	DB	ID	Description
17	47	40.2	644	10	QBLLDV1	Q81dvi arabidopsis
18	47	40.2	644	10	QPFN3	Q9f3k3 arabidopsis
19	47	40.2	1226	16	Q7UJ12	Q9f12 rhodopirell
20	47	40.2	1873	10	Q9FG11	Q9f911 arabidopsis
21	46	39.3	288	12	Q8Z214	Q98214 molluscum C
22	46	39.3	637	5	Q86GJ9	Q86gj9 dictyosteli
23	46	39.3	700	11	Q9CAF5	Q9cx5t mus musculus
24	46	39.3	700	11	Q8C0B3	Q8c0b3 mus musculus
25	46	39.3	781	15	Q82857	Q82857 .lembrana di
26	46	39.3	1283	5	Q8TA02	Q8ta02 caenorhabdi
27	45.5	38.9	95	3	Q8TEF3	Q8tef3 agrocybe ae
28	45	38.9	76	7	Q30734	macaca nem
29	45	38.5	76	7	Q30567	macaca fasc
30	45	38.5	7	7	Q30747	macaca fasc
31	45	38.5	316	16	Q9IJ3	Q9ij3 pseudomonas
32	45	38.5	446	10	Q94CT7	Q9ict oryza sativ
33	45	38.5	479	5	Q9UTPS	Q9utps eurolliculi
34	45	38.5	567	5	Q95RA8	Q95r48 drosophila
35	45	38.5	567	5	Q9VCB3	Q9vc3 drosophila
36	45	38.5	773	16	Q8AC00	Q8aco0 bacteroides
37	45	38.5	968	5	Q7Z247	Q7z247 cryptospori
38	45	38.5	1056	12	Q57161	Q57161 spinach lat
39	44.5	38.0	691	5	Q9VML1	Q9vml1 drosophila
40	44.5	38.0	693	5	Q96680	Q96680 drosophila
41	44.5	38.0	810	10	Q9ZK13	Q9zk13 cucurbita m
42	44	37.6	47	16	Q8XPL2	Q8xpl2 salmonella sp
43	44	37.6	195	16	Q8ZG3	Q8zg3 anaerobea sp
44	44	37.6	606	5	Q9WVF6	Q9wvf6 drosophila
45	44	37.6	2023	12	Q91632	Q91632 cherry tree

## SUMMARIES

## RESULT 1

Score	Query	Match	Length	DB	ID	Description
035545				PRELIMINARY;		PRT; 316 AA.
035545;				AC		
035545;				DT	01-JAN-1998 (TRNMBLrel.	05; Created)
035545;				DT	01-JAN-1998 (TRNMBLrel.	05; Last sequence update)
035545;				DT	01-OCT-2003 (TRNMBLrel.	25; Last annotation update)
035545;				DE	"The intron 5-inserted form of erythropoietin receptor precursor.	
035545;				OS	Rattus norvegicus (Rat).	
035545;				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.	
035545;				RN	[1]	NCBI_TAXID=10116;
035545;				RN		RN
035545;				RP		SEQUENCE FROM N.A.
035545;				RX		MEDLINE:98286111; PubMed=9630610;
035545;				RA		Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H., Miyatake K., Nakano Y.;
035545;				RA		RA
035545;				RT	"The intron 5-inserted form of rat erythropoietin receptor is expressed as a membrane-bound form."	RT
035545;				RL	Blochim. Biophys. Acta 1403:169-178(1998).	RL
035545;				DR	D83509; Bar22373.1; -	DR
035545;				DR	HSSP; P19235; IBSA.	DR
035545;				DR	GO; GO:0016020; C:membrane; IEA.	DR
035545;				DR	GO; GO:0004896; F:hematopoietin/intferon-class (D200-domain. . . IEA.	DR
035545;				DR	GO:1004872; P:receptor activity; IEA.	DR
035545;				DR	InterPro; IPR024872; CRIA.	DR
035545;				DR	InterPro; IPR039361; FN III.	DR
035545;				DR	InterPro; IPR03557; FN III-like.	DR
035545;				DR	InterPro; IPR03528; Hemtopopt L_F1.	DR
035545;				DR	Pfam; PF00041; En3; 1.	DR
035545;				DR	SMART; SM0060; FN3; 1.	DR
035545;				DR	PROSITE; PS01352; HEMATopo_REC_L_F1; 1.	DR
035545;				KW	Receptor; Signal.	KW
035545;				FT	SIGNAL 1 24	FT
035545;				FT	CHAIN 25 316	FT
035545;				SEQUENCE	316 AA; 34220 MW; 05C44BR8516C180B CRC64;	SEQUENCE
035545;					Query Match Score 109; DB 11; Length 316;	
035545;					Best Local Similarity 91.3%; Pred. No. 6.8e-10;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	109	93.2	316	11	Q35545	Q35545 rattus norv	
2	107	91.5	509	6	Q9MYZ9	Q9myz9 sus scrofa	
3	104	88.9	229	6	Q2B206	Q2b206 bos taurus	
4	104	88.9	229	6	Q27950	Q27950 bos indicus	
5	104	88.9	387	6	Q95N13	Q95n13 ovis aries	
6	104	88.9	418	6	Q95N14	Q95n14 ovis aries	
7	56	47.9	176	17	Q8TYF5	Q8tyf5 methanopyru	
8	52	44.4	1028	4	Q9UQ52	Q9uq52 homo sapiens	
9	49	41.9	826	2	Q9AKX8	Q9akx8 legionella	
10	49	41.9	1028	11	P97528	P97528 rattus norv	
11	48	41.0	428	10	Q9LPY7	Q9lp7 arabidopsis	
12	48	41.0	1028	11	Q9JRNB8	Q9jrnbb8 mus musculus	
13	48	41.0	1028	11	Q8C6X1	Q8c6x1 mus musculus	
14	47	40.2	539	10	Q94186	Q94186 oryza sativ	
15	47	40.2	539	10	Q7KDN4	Q7kdn4 oryza sativ	
16	47	40.2	640	10	Q9ASX3	Q9asx3 arabidopsis	

Matches	21;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	QRVILLEGRTECVLNSNLRGRTY	23						
Db	193	QRVVLEGRTECVLNSNLRGRTY	215						
RESULT 2									
Q9MYZ9		PRELIMINARY;		PRT;	509	AA.			
AC	Q9MYZ9;								
DR	01-OCT-2000	(TREMBLrel. 15, Created)							
	01-OCT-2000	(TREMBLrel. 15, Last sequence update)							
	01-OCT-2003	(TREMBLrel. 25, Last annotation update)							
	Erythropoietin receptor.								
OS	Sus scrofa (Pig).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
NCBI_TaxID=9823;	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.								
[1]	RN	SEQUENCE FROM N.A.							
RP	SEQUENCE-Liver;								
RC	Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,								
RA	Christensen R.K., Vallet J.L.;								
RA	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in								
RT	"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in								
RT	Embryonic and Fetal Liver.";								
RT	Domest. Anim. Endocrinol. 0:0-0(2000).								
RL									
DR	EMBL; AP274305; IERN.								
DR	HSSP; P19255; C:membrane; IEA.								
DR	GO; GO:0008996; P:hematopoietin/interferon-class (D200-domain. . . ; IEA.								
DR	GO; GO:004872; P:receptor activity; IEA.								
DR	GO; GO:006118; P:electron transport; IEA.								
DR	InterPro; IPR002896; CRIA.								
DR	InterPro; IPR003961; PN-III.								
DR	InterPro; IPR00857; PN-III-like.								
DR	InterPro; IPR003528; Hemtopoptn_L_F1.								
DR	InterPro; IPR00572; Oxidored_molyb.								
DR	PFam; PF00041; FN3; 1.								
DR	SMART; SM00060; FN3; 1.								
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.								
DR	PROSITE; PS05559; MOLBDOPTERIN_EUK; 1.								
KW	Receptor.								
SEQUENCE	509 AA;	55183 MW;	35B565D07C6BCDBA	CRC64;					
Qy	1	QRVILLEGRTECVLNSNLRGRTY	23						
Db	195	QRVVLEGRTECVLNSNLRGRTY	217						
RESULT 3									
Q28206		PRELIMINARY;		PRT;	229	AA.			
AC	Q28206;								
DR	01-NOV-1996	(TREMBLrel. 01, Created)							
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)							
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)							
DE	Erythropoietin receptor (Fragment).								
GN	EPOR.								
OS	Bos taurus (Bovine).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;								
OC	Bovidae; Bovinae; Bos.								
OX	NCBI_TaxID=9913;								
RN	SEQUENCE FROM N.A.								
RC	TISSUE-Bone marrow.								
RC	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.								
RESULTS	2	1	QRVILLEGRTECVLNSNLRGRTY	23.					
Qy	1	QRVILLEGRTECVLNSNLRGRTY	23						
Db	136	QRVVLEGRTECVLNSNLRGRTY	158						



GO: GO:0007417; P: central nervous system development; TAS.

DR InterPro; IPR003439; ABC transporter.

DR IPR03941; FN\_III.

DR InterPro; IPR008937; FN\_III-like.

DR InterPro; IPR007110; Ig-like.

DR IPR003588; Ig\_c2.

DR Pfam; PF00041; fn1; 4.

DR Pfam; PF00047; Ig\_6.

DR SMART; SM00060; IGC2; 5.

DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.

DR PROSITE; PS50835; Ig\_LIKE; 6.

KW Immunoglobulin domain.

SEQUENCE 1028 AA; 113956 MW;

BB5A2ED2F29936A6 CRC64;

Qy 7 EGRTBCVLSNLRGR 20

Db 292 EGFYECIASNLRGR 305

RESULT 9  
Q9AKX8 PRELIMINARY; PRT; 826 AA.  
ID Q9AKX8; PRELIMINARY;  
AC Q9AKX8; PRELIMINARY;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Legionellaceae; Legionella.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Legionellaceae; Legionella.  
NCBI\_TaxID=446;  
RN [1]  
RP SEQUENCE FROM N.A.

STRAIN=serogroup 1,  
MEDLINEB21150471; PubMed=11551842;  
RX Lujeneberg B., Mayer B., Darby N., Kooststra O., Zaehringer U.,  
RA Rohde M., Swanson J., Prosch M.;  
RT "Chromosomal insertion and excision of a 30 kb instable genetic  
element is responsible for phase variation of lipopolysaccharide and  
other virulence determinants in Legionella pneumophila.";  
RL Mol. Microbiol. 39:1259-1271(2001).  
DR EMBL; AU227755; CRCS3467.1; -.  
KW Hypothetical protein.  
SEQUENCE 826 AA; 91501 MW; 4BD5404C2665CFEF CRC64;

Qy 1 QRVELLEGRTBCVLSNLRGR 21  
Db 782 RRAASNEGGLETLIESLNLRGR 802

Query Match 41.9%; Score 49; DB 2; Length 826;  
Best Local Similarity 42.9%; Pred. No. 25;  
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Query Match 41.9%; Score 48; DB 10; Length 428;  
Best Local Similarity 45.5%; Pred. No. 18;  
Matches 4; Mismatches 8; Indels 0; Gaps 0;

RESULT 10  
P91528 PRELIMINARY; PRT; 1028 AA.  
ID P91528 PRELIMINARY;  
AC P91528 PRELIMINARY;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DB NB-3.  
OC Eukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=Mistar; TISSUE=Brain;  
RX MEDLINE=97101230; PubMed=8945756;  
RA Ogawa J., Kaneko H., Matsuda T., Nagara S., Hosoya H., Watanabe K.;  
RT "Novel neural adhesion molecules in the Contactin/F3 subgroup of the  
immunoglobulin superfamily: Isolation and characterization of cDNAs  
from rat brain." Neurosci. Lett. 218:173-176 (1996).  
RL DR EMBL; DB7248; BA13320.1; -.  
DR GO; GO:001620; Cimembrane; IBA.  
DR GO; GO:000554; F:ATP binding; IBA.  
DR GO; GO:0004009; F:ATP-binding cassette, (ABC) transporter acti...; IBA.  
DR GO; GO:0006810; P:transport; IBA.  
DR InterPro; IPR03439; ABC transporter.  
DR InterPro; IPR03361; FN\_III-like.  
DR InterPro; IPR00857; FN\_III-like.  
DR InterPro; IPR07110; Ig-like.  
DR InterPro; IPR03598; Ig\_c2.  
DR PFAM; PF00041; fn3; 4.  
DR Pfam; PF00047; Ig\_6.  
DR SMART; SM00060; IGC2; 5.  
DR PROSITE; PS00111; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS50835; Ig\_LIKE; 6.  
KW Immunoglobulin domain.  
SQ SEQUENCE 1028 AA; 114065 MW; 47EFD8A370CF4923 CRC64;

RESULT 11  
Q9LPY7 PRELIMINARY; PRT; 428 AA.

ID Q9LPY7 PRELIMINARY;  
AC Q9LPY7 PRELIMINARY;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE T23J18.14.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Buletaria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyra; eudicots; rosids;  
OC euriosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;  
OX [1]  
RN RP SEQUENCE FROM N.A.  
RA Shimamoto P., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafii H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conn A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federer N.A., Theologis A., Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC T23J18 from chromosome I.";  
RT Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AC011651; AACF16632.1; -.  
DR SEQUENCE 428 AA; 48982 MW; 603F3FF2725622F9 CRC64;

Query Match 41.0%; Score 48; DB 10; Length 428;  
Best Local Similarity 45.5%; Pred. No. 18;  
Matches 4; Mismatches 8; Indels 0; Gaps 0;  
SQ SEQUENCE 1 QRVELLEGRTBCVLSNLRGR 22  
Db 132 KRPOLLENTLCLILSITRGSRR 153

RESULT 12

Q9JM88 PRELIMINARY; PRT; 1028 AA.  
 AC Q9JM88;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 GN Neural recognition molecule NB-3.  
 CNTN6 or MNB-3.  
 OS Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C29SVG; TRISUB=Brain;  
 MEDLINEB=20183687; PubMed=10717476;  
 PA Lee S., Takeda Y., Kawano H., Hosoya H., Nomoto M., Fujimoto D.,  
 Takahashi N., Watanabe K.;  
 RT "Expression and regulation of a gene encoding neural recognition  
 molecule NB-3 of the contactin/F3 subgroup in mouse brain.";  
 RL Gene 24:253-266 (2000).  
 CC -!- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 DR EMBL; AE032602; BAA92367.1; -.  
 HSPP; P20241; 1CPB.  
 MGD; MGJ1:18562223; Cntn6.  
 DR GO:0016020; Cmembrane; IEA.  
 GO; GO:0005542; F:ATP binding; IBA.  
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . . ; IEA.  
 DR GO; GO:0006810; P:Transport; IBA.  
 DR InterPro; IPR03439; ABC transporter.  
 DR InterPro; IPR003951; FN III-like.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR07110; Ig-like.  
 DR InterPro; IPR003588; Ig C2.  
 DR PFam; PF00041; fn3; 4.  
 DR PFam; PF00047; Ig; 6.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00409; Ig; 6.  
 DR SMART; SM00408; IgC2; 6.  
 DR PROSITE; PS00211; ABC TRANSPORTER\_1; 1.  
 DR PROSITE; PS500835; Ig\_LIKE; 6.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 SQ SEQUENCE 1028 AA; 113759 MW; B233ED300881B101 CRC64;

Query Match Score 48; DB 11; Length 1028;  
 Best Local Similarity 64.3%; Pred. No. 47;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 14  
 O94LS6 PRELIMINARY; PRT; 539 AA.  
 ID Q94LS6  
 AC Q94LS6;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice).  
 OC Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrartoidea; Oryzeae; Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Cv. Nipponbare;  
 RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Gansberger K.,  
 RA Brenner M., Burgess S., Hance M., Shavartsev M., Tsitkin T.,  
 RA Riggs F., Hsiao J., Zisman V., Blunt S., Pai G., VanAken S.S.,  
 RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSNBB0011A08 genomic sequence.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AC034258; AAK54287.1; -.  
 DR Gramene; Q9AL66;  
 DR Gramene; Q9AL66;  
 KW Hypothetical protein.  
 SQ SEQUENCE 539 AA; 60201 MW; 8EBSD40239310BC2 CRC64;

Query Match Score 47; DB 10; Length 539;  
 Best Local Similarity 56.2%; Pred. No. 34;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 15  
 Q8C6X1 PRELIMINARY; PRT; 1028 AA.  
 ID Q8C6X1  
 AC Q8C6X1;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Contactin 6.  
 GN CNTN6.  
 OS Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Heart;  
 RC MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;

Q7XDN4 PRELIMINARY; PRT; 539 AA.  
ID Q7XDN4 ;  
AC Q7XDN4 ;  
DT 01-OCT-2003 (TREMBrel. 25, Created)  
DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OSJNBB0011A08.11.  
OS Oryza sativa (japonica cultivar-group); Streptophyta; Embryophyta; Tracheophyta;  
Eukaryota; Viridiplantae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoidae; Oryzeae; Oryza.  
NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA The Rice Chromosome 10 Sequencing Consortium;  
RT "In-depth view of structure, activity, and evolution of rice  
RT chromosome 10.";  
RL Science 300:1566-1569 (2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AEO17102; ARP54107.1;  
KW Hypothetical protein.  
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;  
Query Match 40.2%; Score 47; DB 10; Length 539;  
Best Local Similarity 56.2%; Pred. No. 34;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 4 EILFGRTTECVLNLRG 19  
Db : ||| ||| :|||  
9 EVHEGSTRSCVLLNVRG 24

Search completed: May 6, 2004, 12:46:18  
Job time : 40 secs



DR	InterPro; IPRO003961;	FN III.	
DR	InterPro; IPRO03524;	Hemopoietin_L_F1.	
DR	Pfam; PF00041;	fn3;	1.
DR	PIRSF; PIRSF001959;	EPO_receptor;	1.
DR	SMART; SN00066;	FNS_1.	
DR	PROSITE; PS01352;	HEMATopo REC L_F1;	1.
DR	Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;		
KW	3D-structure.		
KW	FT SIGNAL	24	
FT	PT CHAIN	25	508
FT	PT DOMAIN	25	250
FT	PT TRANSMEM	251	273
FT	PT DOMAIN	274	508
FT	PT DOMAIN	148	213
FT	PT SITE	368	368
FT	PT DISULFID	52	62
FT	PT DISULFID	91	107
FT	PT MOD_RES	368	368
FT	PT CARBOHYD	776	76
FT	PT HELIX	33	45
FT	PT STRAND	51	54
FT	PT STRAND	61	66
FT	PT HELIX	73	73
FT	PT HELIX	74	76
FT	PT STRAND	77	83
FT	PT TURN	84	85
FT	PT STRAND	89	90
FT	PT STRAND	94	97
FT	PT TURN	99	100
FT	PT STRAND	103	108
FT	PT HELIX	111	113
FT	PT TURN	116	117
FT	PT STRAND	120	126
FT	PT TURN	127	128
FT	PT STRAND	131	137
FT	PT HELIX	139	141
FT	PT STRAND	143	143
FT	PT TURN	149	155
FT	PT STRAND	162	167
FT	PT TURN	170	171
FT	PT HELIX	175	177
FT	PT STRAND	178	186
FT	PT STRAND	195	198
FT	PT TURN	200	201
FT	PT STRAND	204	207
FT	PT STRAND	215	224
FT	PT TURN	226	228
FT	PT STRAND	231	231
FT	SEQUENCE	240	243
FT	SEQUENCE	508 AA;	55065 MW;
FT	SEQUENCE	1 QRVLEILGEGTCTYLSNLGRTRY	23
FT	SEQUENCE	194 QRVLEILGEGTCTYLSNLGRTRY	216
RESULT 2			
EPOR_MOUSE	STANDARD;		
ID	PI1753;	Q63852;	
AC	P1753;	063852;	
DT	01-APR-1990	(Rel. 14, Created)	
DT	01-APR-1990	(Rel. 14, Last sequence update)	
DT	15-MAR-2004	(Rel. 43, Last annotation update)	
DB	Erythropoietin receptor precursor (EPO-R).		
GN	EPOR.		
OS	Mus musculus (Mouse).		
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M		
NCBI_TaxId=10090;			





DR InterPro; IPR002889; WSC.

DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00051; Kringle; 1.

DR Pfam; PF01822; WSC; 1.

DR PRINTS; PR00018; KRINGLE.

DR PRODOM; PD00395; Kringle; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00130; KR; 1.

DR PROSITE; PS00180; CUB; 1.

DR PROSITE; PS00021; KRINGLE 1; 1.

DR PROSITE; PS50070; KRINGLE 2; 1.

KW Wnt signaling pathway; Signal; Transmembrane; Kringle.

PT SIGNAL 19 POTENTIAL.

PT CHAIN 20 KREMen PROTEIN 1.

PT DOMAIN 21 EXTRACELLULAR (POTENTIAL).

PT DOMAIN 21 CYTOPLASMIC (POTENTIAL).

PT DOMAIN 21 KRINGLE.

PT DOMAIN 21 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT DOMAIN 21 CUB.

PT CARBOHYD 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT CARBOHYD 217 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT CARBOHYD 255 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT CARBOHYD 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT CARBOHYD 333 N-LINKED (GLCNAC. . .) (POTENTIAL).

PT CARBOHYD 345 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 473 AA; 51716 MW; 585827788BE3FDD1 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 473;

Best Local Similarity 55.0%; Pred. No. 4.1;

Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VEILEGRTECVLNSNRGRT 22

Db 268 VELLDGYTRVLYRLSGRSR 287

RESULT 6

KRNL\_HUMAN

ID Q96MU8; STANDARD; PRT; 475 AA.

AC Q9BY70; Q9UGJ1; Q9UGJ1.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).

GN KREMen; OR KREMen.

OS Homo sapiens (Human).

OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A. (ISOFORM 1).

PA Nakamura T.; Nakamura T.; Nakamura T.

RN Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

RN [2] SEQUENCE FROM N.A. (ISOFORM 2).

RA Tashiro H.; Yamazaki M.; Watanabe K.; Kumagai A.; Itakura S.,

RA Pukuyama Y.; Fujimori Y.; Komiyama M.; Sugiyama T.; Irie R.,

RA Oresuki T.; Seto H.; Wakamatsu A.; Ishii S.; Yamamoto J.; Isono Y.,

RA Matsuo K.; Nakamura Y.; Sekine M.; Kituchi H.; Kanda K.; Nagatsuma M.,

RA Murakawa K.; Kaneko K.; Takahashi-Fujii A.; Oshima A.; Sugiyama A.,

RA Isogai T.; Suzuki Y.; Sugano S.; Nagahari K.; Masuho Y.; Nagai K.,

RA Kawakami B.; Suzuki B.; Saito K.; Nishikawa T.; Kimura K.; Yamashita H.,

RA "NEDO human cDNA sequencing project."

RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

RN [3] SEQUENCE FROM N.A.

RP MEDLINE-20051765; PubMed=10591208;

RA Dunham J.; Hunt A.R.; Collins J.B.; Bruskiewich R.; Beare D.M.,

RA Clamp M.; Smink L.J.; Ainscough R.; Almeida J.P.; Babbage A.K.,

RA Baggaley C.; Bailey J.; Barlow K.P.; Bates K.N.; Beasley O.P.,

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SMART; SMART00042; CUB; 1.  
 SMART; SMART00130; KR; 1.  
 PROSITE; PS001180; CUB; 1.  
 PROSITE; PS00021; KRINGLE\_1; 1.  
 PROSITE; PS00070; KRINGLE\_2; 1.  
 Wnt signaling pathway; Signal; Transmembrane; Kringle; 1.  
 KW ALTERNATIVE splicing; POTENTIAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 475  
 FT DOMAIN 21 394  
 FT TRANSMEM 395 415  
 FT DOMAIN 416 475  
 FT DOMAIN 33 116  
 FT DOMAIN 216 202  
 FT DOMAIN 47 47  
 FT CARBOHYD 61 61  
 FT CARBOHYD 219 219  
 FT CARBOHYD 295 295  
 FT CARBOHYD 335 335  
 FT CARBOHYD 347 347  
 FT VARSPLIC 473 475  
 FT CONFLICT 29 30  
 FT CONFLICT 206 206  
 SQ SEQUENCE 475 AA; 51898 MW; B7E86FD80F96A0A4 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 475;  
 Best Local Similarity 50.0%; Pred. No. 4.1;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 Qy 3 VEILEGRTEBCVLSNLRGRT 22.  
 Db 270 VELLDGYTHRVLAREFHGRSR 289

RESULT 7  
 PYRB\_COREF COREF STANDARD; PRT; 312 AA.  
 AC QFRT39;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamoylase) (ATCase).  
 DE PYRB OR CE1742.  
 OS Corynebacterium efficiens.  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13332 / DSM 20300 / NCIB 10025;  
 RA Nagatawa S.;  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13332."  
 RL Submitted MAY 2002 to the EMBL/GenBank/DBJ databases.  
 CC 1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate  
 CC + N-carbamoyl-L-aspartate.  
 CC 1- PATHWAY: Pyrimidine biosynthesis; second step.  
 CC 1- SIMILARITY: Belongs to the ATCase/Ortcase family.

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DR EMBL; AP005219; BAB18542.1; ALT\_INIT.  
 DR HAMAP; MF 00001; "-"; 1.  
 DR InterPro; IPR006130; Asp/Orn\_Cotranf.  
 DR InterPro; IPR000082; Asp-Carbmitransf.  
 DR InterPro; IPR006131; Ortcase\_O.  
 DR InterPro; IPR006132; Ortcase\_P.  
 DR InterPro; IPR006133; Ortcase\_O.  
 DR TIGRFAM; TIGR067; CARBONYLTTRANSFERASE; 1.  
 DR PROTEIN; PS00097; CARBONYLTTRANSFERASE; 1.  
 DR Pyrimidine biosynthesis; Transferase; Complete proteome.  
 DR SEQUENCE 312 AA; 33706 MW; EEP40AAD9841DD3B CRC64;  
 SQ Query Match 41.0%; Score 48; DB 1; Length 312;  
 DR Best Local Similarity 61.1%; Pred. No. 3.7;  
 DR Matches 11; Conservative 1; Mismatches 6; Indels 8  
 DR Gaps 0;  
 DR Pyrimidine biosynthesis; Transferase; Complete proteome.  
 DR SEQUENCE 312 AA; 33706 MW; EEP40AAD9841DD3B CRC64;

RESULT 8  
 PYRB CORGL STANDARD; PRT; 312 AA.  
 AC QBNQ78;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamoylase) (ATCase).  
 DE PYRB OR CGH1612.  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1718;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13332 / DSM 20300 / NCIB 10025;  
 RA Nagatawa S.;  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13332."  
 RL Submitted MAY 2002 to the EMBL/GenBank/DBJ databases.  
 CC 1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate  
 CC + N-carbamoyl-L-aspartate.  
 CC 1- PATHWAY: Pyrimidine biosynthesis; second step.  
 CC 1- SIMILARITY: Belongs to the ATCase/Ortcase family.

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DR EMBL; AP005279; BAB9005.1; -.  
 DR HAMAP; MF 00001; "-"; 1.  
 DR InterPro; IPR006130; Asp/Orn\_Cotranf.  
 DR InterPro; IPR000082; Asp-Carbmitransf.  
 DR InterPro; IPR006131; Ortcase\_O.  
 DR InterPro; IPR006132; Ortcase\_P.  
 DR Pfam; PF001185; Ortcase\_N; 1.  
 DR PR02229; AOTCASE.  
 DR TIGRFAM; TIGR067; TIGR0670; asp\_carb\_tr; 1.

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DR Genome Res. 13:1572-1579 (2003).  
 DR 1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate  
 DR + N-carbamoyl-L-aspartate.  
 DR 1- PATHWAY: Pyrimidine biosynthesis; second step.  
 DR 1- SIMILARITY: Belongs to the ATCase/Ortcase family.

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-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.  
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.  
 SEQUENCE 312 AA; F33154FD033CF22 CRC64;

Query Match Score 48; DB 1; Length 312;  
 Best Local Similarity 61.1%; Pred. No. 3.7; Mismatches 6; Indels 0; Gaps 0;

Qy 4 EILGGRTECYLSNLRGRT 21  
 Db 27 EVLGREVRKPLTRGRT 44

RESULT 9

ID	TSP3_HUMAN	STANDARD	PRT	956 AA.
AC	P9746; Q8WV34;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Thrombospondin 3 precursor.			
GN	TBBS3 OR TSP3.			
OC	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
ON	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Lung			
RX	Medline=96044440; PubMed=7558000;			
RA	Adolph K.W., Long G.L., Wintlefield S., Giinns B.I., Bornstein P.; RT "Structure and organization of the human thrombospondin 3 gene (TBBS3)."; RT Genomics 27:329-336 (1995).			
RL	[2]			
RN	SEQUENCE OF 1-736 FROM N.A.			
RX	Medline=97474796; PubMed=9311372;			
RA	Winfield S.L., Tayebi N., Martin B.M., Giinns B.I., Sidransky E.; RT "Identification of three additional genes contiguous to the glucocerebrosidase locus on chromosome 1q21: implications for Gaucher disease."; RT Genome Res. 7:1020-1026 (1997).			
RL	[3]			
RN	SEQUENCE OF 365-956 FROM N.A.			
RP	TISSUE=Retina;			
RC	Medline=23088257; PubMed=12477932;			
RX	Klausner R.L., Feingold B.A., Grouse L.H., Derge J.G., Shemmen C.M., Schuler G.D., Altschul S.P., Collins P.S., Wagner J., Shemmen C.M., Schuler G.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hsieh F., Villanova D.K., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Pahey J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Brownstein M.J., Usdin T.B., Yoshihiko S., Carninci P., Prange C., Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villanova D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rodriguez A.C., Grimmwood J., Schmitz J., Myers R.M., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A., Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type v collagen.			
CC	-!- SUBUNIT: Oligomer; disulfide-linked.			
CC	-!- SIMILARITY: Belongs to the thrombospondin family.			
CC	-!- SIMILARITY: Contains 4 EGF-like domains.			
CC	-!- SIMILARITY: Contains 7 TSP type-3 domains.			

DR EMBL; L38969; AAC41762.1; -.  
 DR EMBL; AP032268; AAC51818.1; -.  
 DR EMBL; BC018786; AAH18786.1; -.  
 DR PIR; A57121; A57121.  
 DR HSSP; P3555; IEMN.  
 DR Geneva; HGNC:11787; TBBS3.  
 DR MIM; 188062; -.  
 DR GO; GO:0005509; F:calcium ion binding; TAS.  
 DR GO; GO:0001610; P:cell-matrix adhesion; TAS.  
 DR InterPro; IPR01881; EGF\_Ca.  
 DR InterPro; IPR062209; EGF\_Like.  
 DR InterPro; IPR03367; tsp\_3.  
 DR InterPro; IPR08859; TSPC.  
 DR InterPro; IPR03129; TSPN.  
 DR Pfam; PF00008; BGP; 1.  
 DR Pfam; PF02412; tdp\_3; 13.  
 DR Pfam; PF05735; TSPC; 1.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMAP; SH00210; TSPN; 1.  
 DR PROSITE; PS00032; BGP; 1; FALSE\_NEG.  
 DR PROSITE; PS01186; BGP; 2; 1.  
 DR PROSITE; PS00036; EGF\_3; 1.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGP-Like domain; Signal.  
 KW SIGNAL 1 21  
 PT CHAIN 22 956  
 PT DOMAIN 22 272  
 PT DOMAIN 274 315  
 PT DOMAIN 316 369  
 PT DOMAIN 370 413  
 PT DOMAIN 414 456  
 PT DOMAIN 488 523  
 PT DOMAIN 524 546  
 PT DOMAIN 547 582  
 PT DOMAIN 583 605  
 PT DOMAIN 606 643  
 PT DOMAIN 644 683  
 PT DOMAIN 684 719  
 PT DOMAIN 720 956  
 PT DISUFD 266 266  
 PT DISUFD 269 269  
 PT DISUFD 344 368  
 PT DISUFD 374 388  
 PT DISUFD 283 300  
 PT DISUFD 303 314  
 PT DISUFD 320 332  
 PT DISUFD 326 341  
 PT DISUFD 344 368  
 PT DISUFD 426 442  
 PT DISUFD 444 455  
 PT DISUFD 471 478  
 PT DISUFD 483 503  
 PT DISUFD 519 539  
 PT DISUFD 542 562  
 PT DISUFD 578 598  
 PT DISUFD 601 621  
 PT DISUFD 639 659  
 PT DISUFD 679 679

FT	DISULFID	715	936	BY SIMILARITY.		PRT;	67 AA.
FT	CARBOHYD	310	310	N-LINKED (GLCNAC. . ) (POTENTIAL).			
FT	CARBOHYD	407	407	N-LINKED (GLCNAC. . ) (POTENTIAL).			
FT	CARBOHYD	644	644	N-LINKED (GLCNAC. . ) (POTENTIAL).			
FT	CARBOHYD	937	937	N-LINKED (GLCNAC. . ) (POTENTIAL).			
SQ	SEQUENCE	956 AA;	104201 MW;	AE9B13D0F0F5B8 CRC64;			
OS	Kluyveromyces lactis (Yeast).						
OS	Bakterien; Fungi; Ascomycota; Saccharomycotina; Kluyveromyces.						
OS	Saccharomycetaceae; Kluyveromyces.						
OS	RPS28.						
OS	Kluyveromyces lactis (Yeast).						
OS	Bakterien; Fungi; Ascomycota; Saccharomycotina; Kluyveromyces.						
OS	Saccharomycetaceae; Kluyveromyces.						
ID	RS28_KLULIA						
AC	P33285;						
DT	01-FEB-1994 (Rel. 28, Created)						
DT	01-FEB-1994 (Rel. 28, Last sequence update)						
DT	15-DEC-1998 (Rel. 37, Last annotation update)						
DB	40S ribosomal protein S28 (S33).						
GN	RPS28.						
RN	SEQUENCE FROM N.A.						
RN	MEDLINE=93127729; PubMed=1481571;						
RN	NCBI_TAXID=28985;						
RX	"Structure and expression of the ABFI-regulated ribosomal protein S33						
RA	Hoekstra R., Ferreira P.M., Bootsma T.C., Mager W.H., Planta R.J.;						
RT	"Structure and expression of the ABFI-regulated ribosomal protein S33						
RT	gene in Kluyveromyces."						
RT	yeast 8:949-959 (1992).						
RL	-1- SIMILARITY: Belongs to the S28B family of ribosomal proteins.						
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CC	EMBL: CAA59296_1; -.						
DR	XG9582; CAA59296_1; -.						
DR	PIR: S30005; S30005.						
DR	InterPro: IPR00289; Ribosomal_S28e.						
DR	PFam: PF01200; Ribosomal_S28e; 1.						
DR	Prosite: PS00541; Ribosomal_S28e; 1.						
DR	Ribosomal protein.						
SQ	SEQUENCE 67 AA; 7536 MW; E5F148312B08A131 CRC64;						
Query Match	Score 46; DB 1; Length 67;						
Best Local Similarity	42.9%; Pred. No. 1.4;						
Matches	9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;						
CC	RESULT 12						
CC	RS28_KLUMA						
CC	STANDARD:						
CC	PRT;						
CC	67 AA.						
CC	AC P33286;						
CC	DT 01-FEB-1994 (Rel. 28, Created)						
CC	DT 01-FEB-1994 (Rel. 28, Last sequence update)						
CC	DT 16-OCT-2001 (Rel. 40, Last annotation update)						
CC	DE 40S ribosomal protein S28 (S33).						
CC	RPS28.						
CC	Kluyveromyces marxianus (Yeast) (Kluyveromyces fragilis).						
CC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Kluyveromyces.						
CC	Saccharomycetaceae; Kluyveromyces.						
CC	RN [1] _TAXID=4911;						
CC	SEQUENCE FROM N.A.						
CC	MEDLINE=93127739; PubMed=1481571;						
CC	"Structure and expression of the ABFI-regulated ribosomal protein S33						
CC	gene in Kluyveromyces."						
CC	yeast 8:949-959 (1992).						
CC	-1- SIMILARITY: Belongs to the S28B family of ribosomal proteins.						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						
CC	EMBL: AE016956; AA082551_1; -.						
DR	TIGR: EF2859;						
DR	HAMAP: MF_00718; -; 1.						
DR	InterPro: IPR004370; Taut.						
DR	Pfam: PF01361; Tautomerase; 1.						
DR	ProDom: PD04143; Taut; 1.						
KW	Isomerase; Complete Proteome.			BY SIMILARITY.			
FT	INIT_MET 0			CATALYTIC BASE (BY SIMILARITY).			
FT	ACT_SITE 1						
SQ	SEQUENCE 58 AA; 6589 MW;			FAE19AO05D93CB4E CRC64;			
Query Match	Score 46; DB 1; Length 58;						
Best Local Similarity	40.0%; Pred. No. 1.2;						
Matches	9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;						
CC	RESULT 17						
CC	VEILLEGRTECVLSNL 17						
CC	5 VELIEGRTEEVQTM 19						
CC	RESULT 11						
CC	RS28_KLULIA						

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CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the cytochrome P450 family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC
CC DR EMBL; X65583; CAA4297.1; -
CC DR S30006; S30006;
CC DR PIR; IPR00289; Ribosomal_S28e.
CC DR Pfam; PF0100; Ribosomal_S28e; 1.
CC DR Prosite; PD005541; Ribosomal_S28e; 1.
CC DR PROSITE; PS00061; RIBOSOMAL_S28E; 1.
CC KW RIBOSOMAL protein.
CC
CC Query Match 39.3%; Score 46; DB 1; Length 67;
CC Best Local Similarity 42.9%; Pred. No. 1.4;
CC Matches 9; Conservative 4; Nisimatches 8; Indels 0; Gaps 0;
CC
CC Qy 2 RVEILEGRTECVLSNLRGTR 22
CC Db 29 RVEFLEDTTIVRNKGPRV 49
CC
CC
CC RESULT 13
CC C128 MYCTU STANDARD; PRT; 489 AA.
CC ID C128_MYCTU STANDARD; PRT; 489 AA.
CC
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 10-APR-2003 (Rel. 42, Last annotation update)
CC DE Putative cytochrome P450 128 (EC 1.14.-.-)
CC GN CYP128 OR RV2268C OR MTcY339.42 OR MBB2291C.
CC OS Mycobacterium tuberculosis, and
CC Bacteria: Actinobacteria: Actinomycetales;
CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CC NCBI_TaxID=1773, 1765;
CC
CC RN
CC RP SEQUENCE FROM N.A.
CC SPECIES:M.tuberculosis; STRAIN=H37Rv;
CC MEDLINE=98295987; PubMed=9634230;
CC RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
CC RA Gordon S.V., Bigmeier K., Gas S., Barry C.E. III, Tekaiwa F.,
CC RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
CC RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N.,
CC RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
CC RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
CC RA Rutledge S., Seeger K., Skelton S., Squares S., Squares R.,
CC RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
CC RT "Deciphering the biology of Mycobacterium tuberculosis from the
CC RT complete genome sequence." Nature 393:537-544(1998).
CC [1]
CC RN
CC RP SEQUENCE FROM N.A.
CC SPECIES:M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
CC MEDLINE=22206494; PubMed=1218036;
CC RA Pleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
CC RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haff D., Hickie E.,
CC RA Kolonay J.F., Nelson W.C., Umayam L.A., Brimholtaeva M., Salzberg S.L.,
CC RA Delcher A., Utterback T., Waidman J., Khouri H., Gill J., Mikula A.,
CC RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M./, Wheeler P.R.,
CC RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
CC RT laboratory strains." J. Bacteriol. 184:5479-5490(2002).
CC [2]
CC RN
CC RP SEQUENCE FROM N.A.
CC SPECIES:M.bovis; STRAIN=AF2122/97;
CC MEDLINE=222070107; PubMed=12188972;
CC RA Garnier T., Bigmeier K., Camus J.-C., Medina N., Mansoor H.,
CC RA Pyor M., Dutchoy S., Grondin S., Lacroix C., Monsempé C., Simon S.,
CC RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
CC RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
CC RT "The complete genome sequence of Mycobacterium bovis." Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC [3]
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CC DR Z77163; CAB00967.1; -
CC DR EMBL; AR007076; ARK46612.1; -
CC DR BX248342; CAD97152.1; -
CC DR PTR; H70729; H70729.
CC DR HSSP; Q00441; 10XA.
CC DR TIGR; MR2330; -
CC DR Tuberculist; RV2268C; -
CC DR InterPro; IPR001128; Cytochrome_P450.
CC DR PRINTS; PR00385; P450.
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC DR Hypothetical protein; Oxidoreductase; Monooxygenase; Heme;
CC KW Transmembrane; Complete Proteome.
CC FT TRANSMEM 207 227 POTENTIAL.
CC FT TRANSMEM 256 276 POTENTIAL.
CC FT TRANSMEM 315 335 POTENTIAL.
CC FT TRANSMEM 383 403 POTENTIAL.
CC FT METAL 435 435 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SQ SEQUENCE 489 AA; 53313 MW; 633P233CEP03AD7A CRC64;
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CC Best Local Similarity 47.6%; Pred. No. 13;
CC Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
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CC Qy 2 RVEILEGRTECVLSNLRGTR 22
CC Db 458 RIEVVEPPPTWNTANLRLGLTR 478
CC
CC
CC RESULT 14
CC AMS2 SCHPO STANDARD; PRT; 697 AA.
CC ID AMS2 SCHPO STANDARD; PRT; 697 AA.
CC AC Q9P721; Q9P721;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE CENP-A multicopy suppressor protein 2.
CC GN AMS2 OR SPCC290_04 OR SPCCCP11_01.
CC OS Schizosaccharomyces pombe (Fission yeast).
CC OC Schizosaccharomyces pombe (Fission yeast).
CC OC Schizosaccharomyces pombe (Schizosaccharomyces);
CC OC Schizosaccharomyces pombe (Schizosaccharomyces);
CC NCBI_TaxID=4896;
CC
CC
CC RN
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=727;
CC RX MEDLINE=21848401; PubMed=11859360;
CC RA Wood V., Gwilliam R., RaJaundream M.A., Lyne M., Lyne R., Stewart A.,
CC RA Seguros J., Peat N., Hayles J., Basham D., Bowman S.,
CC RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
CC RA Collins M., Connor R., Cronin A., Davis P., Peitwell T., Fraser A.,
CC RA Gentle S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgeson G.,
CC RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
CC RA James K., Jones L., Jones M., Leathier S., McDonald S., McLean J.,
CC RA Mooney P., Moule S., Murphy L., Niblett D., Odell C.,
CC RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch B.,
CC RA Rutherford K., Rutter S., Saunders D., Seeger K., Stevens S.,
CC RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
CC RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
CC RA Woodward J., Volkstaert G., Aert R., Robben J., Grymonpre B.,
CC RA Weltjens I., Vanstreels B., Rieser M., Schaefer M., Mueller-Auer S.,
CC RA Gabel C., Fuchs M., Pritz C., Holzer E., Moestl D., Hilbert H.,
CC
CC

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RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 Eger P., Zimmermann W., Wedder H., Wanburtt R., Purnelle B.,  
 Goffeau A., Cadieu E., Dreano S., Gloux S., Lejaire V., Mottier S.,  
 Golbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 Spakowski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.",  
 Nature 415:871-880(2002).  
 RL [2]  
 RN FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=22423783; PubMed=12335531;  
 RA Chen E.S., Saitoh S., Yanagida M., Takahashi K.;  
 RT "A cell cycle-regulated GATA factor promotes centromeric localization  
 of CENP-A in fission yeast.",  
 RL Cell 11:175-187 (2003).  
 I- FUNCTION: Required for proper chromosome segregation via  
 regulation of CENP-A localization to the centromere.  
 CC -|- FUNCTION: Interacts with CENP-A.  
 CC -|- SUBCELLULAR LOCATION: Nuclear, centromeric.  
 CC -|- SIMILARITY: Contains 1 GATA-type zinc finger.  
 CC -|-  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 of CENP-A in fission yeast.";  
 CC -|- FUNCTION: Required for proper chromosome segregation via  
 regulation of CENP-A localization to the centromere.  
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 CC -|- SIMILARITY: Contains 1 GATA-type zinc finger.  
 CC -|-  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 of CENP-A in fission yeast.";  
 CC -|- FUNCTION: Required for proper chromosome segregation via  
 regulation of CENP-A localization to the centromere.  
 CC -|- SIMILARITY: Contains 1 GATA-type zinc finger.  
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 DR GeneDB; All117389; CAB55767.2; .  
 DR GeneDB; SPombe; SPC290.04; .  
 DR GO; GO\_0005694; C:chromosome; ISS.  
 DR GO; GO\_0005654; C:nucleoplasm; ISS.  
 DR GO; GO\_0007049; P:cell cycle; ISS.  
 DR InterPro; IPR000679; Zinc\_GATA.  
 DR PROSITE; PS00344; GATA\_ZN\_FINGER\_1; FALSE\_NEG.  
 DR PROSITE; PS00114; GATA\_ZN\_FINGER\_2; 1.  
 DR Transcription regulation; Nuclear protein; Centromere; DNA-binding;  
 KW Zinc-finger.  
 FT ZN\_FINGER 351 378 GATA-TYPE (ATYPICAL).  
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RESULT 15  
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 ID YL54\_CAEEL  
 AC P34434;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein F44E2.4 in Chromosome III.  
 DE F44E2.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chronadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditida; Pejoderaiae; Caenorhabditis.  
 NCBI TaxID=6239;  
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 MEDLINE=94150718; PubMed=7906398;  
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hypothetical prote	T49830	231	2
transposase (orf2)	A97777	255	2
degenerate transpo	C98084	260	2
esterase seripe -	S75226	283	2
hypothetical prote	D89785	322	2
aspartate-semialde	JQ0198	365	2
1S1167, transposas	1S1168	418	2
1S1167, transposas	B95197	418	2
1S1167, transposas	B95146	418	2
IS1167, transposas	H9518	418	2
thiamin biosynthes	T46944	35.9	2
thiamin biosynthes	AI0554	482	2
inward rectifier p	T29652	514	2
hydrogenase ramula	E70399	562	2
GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
4 protein - protein search, using sw model			
run on: May 6, 2004, 12:44:02 ; Search time 21 Seconds			
(without alignments)			
105,353 Million cell updates/sec			
title: US-10-612-885A-1			
perfect score: 117			
Sequence: 1 QRVTEILLEGRTECVLSNLGRTRY 23			
scoring table: BLOSUM62			

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First-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries						
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<b>Pred.</b> No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
<b>SUMMARIES</b>						
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1	117	100.0	508	1	ZDUR	erythropoietin receptor precursor - human
2	109	93.2	265	2	SI14081	C;Species: Homo sapiens (man)
3	109	93.2	507	1	A32385	C;Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999
4	109	93.2	507	1	A46713	C;Accession: A43799; A60160; A49824; A55280; I52563
5	47	40.2	956	1	A57121	R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
6	46	39.3	67	2	S30006	Blood 76, 31-35, 1990
7	46	39.3	67	2	T30648	A;Title: The gene for the human erythropoietin receptor: analysis of the codin
8	46	39.3	288	2	H70729	A;Reference number: A60160; MUID: 90304334; PMID: 2163695
9	46	39.3	489	1	T41352	A;Accession: A60160
10	46	39.3	710	2	S44821	A;Status: not compared with conceptual translation
11	46	39.3	1609	2	A82639	A;Cross-references: GB: S45332; NID: 9255496; PIDN: AAB23271.1; PID: 9255497
12	45.5	38.9	607	1	A82406	R;Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
13	45	38.5	316	2	D70506	Blood 76, 24-30, 1990
14	45	38.5	512	1	C95184	A;Title: Human erythropoietin receptor cloning, expression, and biologic char
15	45	38.5	1036	2	S22383	A;Reference number: A43799; MUID: 90304334; PMID: 2163695
16	44	38.0	810	2	T4430	A;Molecule type: mRNA
17	44	37.6	47	2	AB0673	A;Residues: 1-101 'R', 103-188 'RP', 191-243 'B', 245-508 <WIN>
18	44	37.6	195	2	AE1823	R;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.
19	43	36.8	84	2	C97995	Blood 78, 2548-2556, 1991
20	43	36.8	408	2	A87649	A;Title: Cloning of the human erythropoietin receptor gene.
21	43	36.8	418	2	I51167	A;Reference number: A53958; MUID: 91372359; PMID: 1654273
22	43	36.8	418	2	F95096	A;Accession: A53958
23	43	36.8	654	2	S76870	A;Molecule type: DNA
24	43	36.8	931	2	S66574	A;Residues: 1-17 'S81-387 'LUSQODDA', 391-395 '504-508 <PEN>
25	43	36.8	956	1	A66116	A;Note: sequence modified after extraction from NCBI backbone
26	43	36.8	1437	2	T31093	A;Note: an insert translated the codon GAT for residue 31 as B
27	42.5	36.3	228	2	H71251	A;Title: Genomic organization of the human erythropoietin receptor gene.
28	42.5	36.2	1894	2	C54689	R;Mauchle, L.; Tournamille, C.; Boffe, G.; Carron, J.P.; Chretien, B.;Hattab, C.,
29	42.5	36.3	1912	2	A56178	Blood 78, 2557-2563, 1991
						A;Title: Cloning of the gene encoding the human erythropoietin receptor.

A; Reference number: I52563; MUID:92399734; PMID:1668607  
 A; Accession: I52563 ;  
 A; Status: translated from GB/EMBL/DDBJ  
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 A; Residues: 1-96 <RES>  
 A; References: GB:M76595; NID:9182147; PIDN:AAA2393.1; PID:9553281  
 C; Genetics:  
 C; Gene: GDB:EPOR  
 A; Cross-references: GDB:125242; OMIM:133171  
 A; Map position: 19013-3-19P13.2  
 A; Introns: 39/1; 84/2-143/1; 195/3; 247/1; 276/2; 305/3  
 A; Superfamily: erythropoietin receptor; cytokine receptor homology  
 C; Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
 P; 1/24/Domain: signal sequence #status predicted <SIG>  
 F; 1/24/Domain: erythropoietin receptor #status predicted <MAP>  
 F; 1/25/250/Domain: extracellular #status predicted <EXT>  
 F; 1/25/239/Domain: cytokine receptor homology <CRS>  
 F; 1/23/WSXWS motif  
 F; 1/25/1-272/Domain: transmembrane #status predicted <TMN>  
 F; 1/27/3-508/Domain: intracellular #status predicted <INT>  
 F; 1/27/1-107/Disulfide bonds: #status predicted  
 F; 1/26/Binding site: carbohydrate (Asn) (covalent) #status predicted  
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 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 194 ORVIELLEGRTECVLSNLRGTRY 216

RESULT 2  
 S14081 erythropoietin receptor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C;Accession: S14081; I49653  
 R; Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
 J. Mol. Biol. 216, 567-575, 1990  
 A;Title: Characterization of murine erythropoietin receptor genes.  
 A;Reference number: S13249; MUID:91080149; PMID:2175360  
 A;Status: preliminary  
 A;Accession: I49653  
 A;Molecule type: DNA  
 A; Residues: 1-465 <RES>  
 A; Cross-references: GB:MG62360; NID:9193199; PIDN:AAA37582.1; PID:g193200  
 C;Superfamily: erythropoietin receptor; cytokine receptor homology  
 C;Keywords: cytokine receptor; transmembrane protein  
 F; 1/25/238/Domain: cytokine receptor homology <CRS>  
 Query Match 93.2%; Score 109; DB 2; Length 265;  
 Best Local Similarity 91.3%; Pred. No. 2.3e-09; Indels 0; Gaps 0;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ORVIELLEGRTECVLSNLRGTRY 23  
 Db 193 ORVIELLEGRTECVLSNLRGTRY 215

RESULT 3  
 A32385 erythropoietin receptor precursor, membrane-bound form - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 28-Sep-1990 #sequence\_revision 05-Apr-1995 #text\_change 22-Jun-1999

C;Accession: A41686; A32385; S13249  
 R;Hino, M.; Tojo, A.; Misawa, Y.; Mori, H.; Takaku, F.; Shibuya, M.  
 Mol. Cell. Biol. 11, 5327-5333, 1991  
 A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
 A;Reference number: A41686; MUID:92017832; PMID:1656233  
 A;Accession: A41686  
 A;Molecule type: mRNA  
 A;Residues: 1-507 <HIN>  
 A;Cross-references: GB:S59368; PIDN:AAB20029.1; PID:9237037  
 A;Experimental source: murine erythroleukemia (MEL) cell line F5-5  
 R;D'Andrea, A.D.; Iodish, H.F.; Wong, G.G.  
 Cell 57, 277-285, 1989  
 A;Title: Expression cloning of the murine erythropoietin receptor.  
 A;Reference number: A32385; MUID:89195338; PMID:2539263  
 A;Accession: A32385  
 A;Molecule type: mRNA  
 A;Residues: 1-507 <DAA>  
 A;Cross-references: GB:J04843; PIDN:AAA37571.1; PID:g30219  
 A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745  
 R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
 J. Mol. Biol. 216, 567-575, 1990  
 A;Title: Characterization of murine erythropoietin receptor genes.  
 A;Reference number: S13249; MUID:91080149; PMID:2175360  
 A;Accession: S13249  
 A;Molecule type: DNA; mRNA  
 A;Cross-references: EMBL:X53081; NID:500861; PIDN:CAA37248.1; PID:g50862  
 A;Experimental source: murine erythroleukemia K-1 cells  
 C;Superfamily: erythropoietin receptor; cytokine receptor homology  
 C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
 C;Genetics:  
 C;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
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 F; 25/507/Product: erythropoietin receptor #status predicted <EXT>  
 F; 25/249/Domain: extracellular #status predicted <EXT>  
 F; 52/238/Domain: cytokine receptor homology <CRS>  
 F; 250/271/Domain: transmembrane #status predicted <TMN>  
 F; 272/507/Domain: intracellular #status predicted <INT>  
 F; 52/62/20-106/Disulfide bonds: #status predicted  
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 Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
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 Qy 1 ORVIELLEGRTECVLSNLRGTRY 23  
 Db 193 ORVIELLEGRTECVLSNLRGTRY 215

RESULT 4  
 A46713 erythropoietin receptor precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C;Accession: A46713  
 R;Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Tabira, T.; Sasaki J. Biol. Chem. 268, 11208-11216, 1993  
 A;Title: Function of erythropoietin receptor of the cells with neural characteristics. C  
 A;Reference number: A46713; MUID:93266574; PMID:7684373  
 A;Accession: A46713  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-507 <MAS>  
 A;Cross-references: GB:D13566; NID:9286209; PIDN:BAA02761.1; PID:9286210  
 A;Experimental source: PC12 and erythroid cells  
 A;Note: Sequence extracted from NCBI backbone (NCBIN:132811, NCBIIP:132813)  
 C;Superfamily: erythropoietin receptor; cytokine receptor homology  
 C;Keywords: cytokine receptor; glycoprotein; transmembrane protein  
 F; 1/24/Domain: signal sequence #status predicted <SIG>  
 F; 25/507/Product: erythropoietin receptor #status predicted <EXT>  
 F; 25/238/Domain: extracellular #status predicted <EXT>  
 F; 52/238/Domain: cytokine receptor homology <CRS>

P:250-271/Domain: transmembrane #status predicted <TMM>  
P:272-507/Domain: intracellular #status Predicted <INT>  
P:15/Binding site: carbohydrate (Asn) (covariant) #status Predicted

Query Match Score 109; DB 1; Length 507;  
Best Local Similarity 91.3%; Pred. No. 4.6e-09;  
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRVVILGGTECVLSNLRGTRY 23  
Db 193 QRVEVLEGGTECVLSNLRGTRY 215

RESULT 5  
A57121  
 ribbospondin 3 precursor - human |  
C:Species: Homo sapiens (man)  
C:Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: A57121; T08830  
R:Adolph, K.W.; Long, G.L.; Winfield, S.; Ginnis, B.I.; Bornstein, P.  
Genomics 27, 329-336, 1995  
A:Title: Structure and organization of the human thrombospondin 3 gene (THBS3).  
A:Reference number: A57121; MUID:96044440; PMID:7556000  
A:Accession: A57121  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-956 <ADD>  
A:Cross-references: GB:L38969; NID:9886298; PIDN: AAC41762.1; PID:98862299; GB:L38970  
R:Winfield, S.L.; Taybi, N.; Martin, B.M.; Giannis, B.I.; Sidransky, E.  
Genome Res. 7, 1020-1026, 1997  
A:Title: Identification of three additional genes contiguous to the glucocerebrosidase 1  
A:Reference number: Z16482; MUID:9331372  
A:Accession: T08830  
A:Status: translated from GB/EMBL/DDJB  
A:Molecule type: DNA  
A:Residues: 1-736 <WIN>  
A:Cross-references: EMBL:AF023268; NID:92564910; PIDN: AAC51818.1; PID:92564912  
C:Genetics:  
A:Gene: GDB:THBS3  
A:Cross-references: GDB:409953; OMIM:188062  
A:Map position: 1q21-1q23  
A:Introns: 27/1; 961/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3; 48  
C:Function:  
A:Description: mediates cell-to-matrix and cell-to-cell interactions  
C:Superfamily: thrombospondin 3; EGF homology  
P:374-412/Domain: EGF homology <EGF>  
Query Match Score 47; DB 2; Length 956;  
Best Local Similarity 45.5%; Pred. No. 4.1e-09;  
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QRVVILGGTECVLSNLRGTRY 22  
Db 113 QOAGLADGRHTVLLRGPSR 134

RESULT 6  
S30006  
 ribosomal protein S28,e - yeast (Kluyveromyces marxianus) |  
N:Alternate names: ribosomal protein YS33  
C:Species: Kluyveromyces marxianus  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999  
C:Accession: S30006  
R:Hoeckstra, R.; Ferreira, P.M.; Bootsma, T.C.; Mager, W.H.; Planta, R.J.  
Yeast 8, 949-955, 1992  
A:Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in K.  
A:Reference number: S30005; MUID:93127729; PMID:1481571  
A:Accession: S30006  
A:Molecule type: DNA  
A:Residues: 1-67 <HOB>  
A:Cross-references: GB:S53420  
C:Genetics:  
A:Gene: S33  
C:Superfamily: rat ribosomal protein S28  
C:Keywords: protein biosynthesis; ribosomes

RESULT 7  
S30005  
 ribosomal protein S28,e - yeast (Kluyveromyces marxianus var. lactis) |  
N:Alternate names: ribosomal protein YS33  
C:Species: Kluyveromyces marxianus var. lactis; Candida sphaerica  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999  
C:Accession: S30005  
R:Hoeckstra, R.; Ferreira, P.M.; Bootsma, T.C.; Mager, W.H.; Planta, R.J.  
Yeast 8, 949-955, 1992  
A:Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in K.  
A:Reference number: S30005; MUID:93127729; PMID:1481571  
A:Accession: S30005  
A:Molecule type: DNA  
A:Residues: 1-67 <HOB>  
A:Cross-references: GB:S53420  
C:Genetics:  
A:Gene: S33  
C:Superfamily: rat ribosomal protein S28  
C:Keywords: protein biosynthesis; ribosomes

Query Match Score 46; DB 2; Length 67;  
Best Local Similarity 42.9%; Pred. No. 3.7%;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 RVBILGGTECVLSNLRGTRY 22  
Db 29 RVEFLIEDTRCTIVRNKGPSR 49

RESULT 8  
T30648  
 probable DNA-binding protein 46L - Molluscum contagiosum virus 1 |  
N:Alternate names: MC046L  
C:Species: Molluscum contagiosum virus 1  
C:Accession: T30648  
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.  
Science 273, 813-815, 1996  
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re  
A:Reference number: Z20876; MUID:96325459; PMID:8670425  
A:Accession: T30648  
A:Status: preliminary; translated from GB/EMBL/DDJB  
A:Molecule type: DNA  
A:Residues: 1-38 <SBN>  
A:Cross-references: EMBL:U60315; NID:91491943; PIDN: AAC55174.1; PID:91491989  
C:Genetics:  
A:Gene: MC046L  
C:Superfamily: DNA-binding phosphoprotein, vaccinia I3L type  
C:Keywords: DNA binding

Query Match Score 46; DB 2; Length 288;  
Best Local Similarity 66.7%; Pred. No. 17%;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 11 ECVLSNLRGTRY 22  
Db 133 ECYTNLRGTRY 144

RESULT 9  
H70729

cytochrome P450 Rv2268c - Mycobacterium tuberculosis (strain H37RV)  
 N; Contains: Oxidoreductase (EC 1.1.-.-.-)  
 C; Species: Mycobacterium tuberculosis  
 C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C; Accession: H70729  
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Peitwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A; Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A; Reference number: A70500; MUID: 98225987; PMID: 9634230  
 A; Accession: H70729  
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Cross-references: GB:Z77163; GB:AL123456; NID:G3261610; PIDN:CAB00967.1; PID:91449352  
 A; Experimental source: strain H37RV  
 C; Genetics:  
 A; Gene: Rv2268c  
 C; Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology  
 C; Keywords: Oxidoreductase  
 F; 322-457/Domain: cytochrome P450 homology <P45>  
 Query Match 39.3%; Score 46; DB 1; Length 489;  
 Best Local Similarity 47.6%; Pred. No. 29;  
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 Qy 2 RVEELGRGPBCVLSNLNRGTR 22  
 Db 458 RIEVEBPPTWTTNANLNRGTR 478

RESULT 10  
 T41352  
 Probable transcription regulator - fission yeast (Schizosaccharomyces pombe) (fragment)  
 C; Species: Schizosaccharomyces pombe  
 C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 R; Barrell, B.G.; Rajandream, M.A.; Quail, M.; Harris, D.; Lyne, M.  
 Submitted to the EMBL Data Library, June 1999  
 A; Reference number: Z21814  
 A; Accession: T41352  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Cross-references: EMBL:AL117389; PIDN:CA855767.1; GSPDB:GN00068; SPDB:SPCC4F11.01  
 A; Experimental source: strain 972h-; cosmid c4F11  
 C; Genetics:  
 A; Gene: SPCC4F11.01  
 A; Map position: 3

Query Match 39.3%; Score 46; DB 2; Length 710;  
 Best Local Similarity 40.3%; Pred. No. 43;  
 Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QRVLELGRGPBCVLSNLNRGTR 22  
 Db 325 EQVRIARGRTEKKFTNVGRGTR 346

RESULT 11  
 S4421  
 F4B2.4 protein - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Aug-1998  
 C; Accession: S44821  
 R; Anderson, K.  
 Submitted to the EMBL Data Library, September 1993  
 A; Description: Sequence of the C. elegans cosmid F44E2.  
 A; Reference number: S44821  
 A; Accession: S44821  
 A; Status: preliminary

A; Molecule type: DNA  
 A; Residues: 1-1609 <AND>  
 A; Cross-references: EMBL:123646; NID:G308595; PIDN:G9388601  
 C; Genetics:  
 A; Introns: 107/2; 173/2; 228/3; 594/3; 1165/2; 1216/3; 1231/3; 1258/2; 1300/2; 1321/3; 1  
 C; Superfamily: LDL receptor ligand-binding repeat homology <LDL>  
 F; 11-45/Domain: LDL receptor ligand-binding repeat homology  
 Query Match 39.3%; Score 46; DB 2;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 ILEGRTECVLSN 16  
 Db 877 ILEGRTECVSS 888

RESULT 12  
 S42639  
 ATP-dependent RNA helicase DB10 - wood tobacco  
 C; Species: Nicotiana sylvestris (wood tobacco)  
 C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Jan-2001  
 C; Accession: S42639  
 R; Itadani, H.; Sugura, M.  
 Plant Mol. Biol. 24, 249-255, 1994  
 A; Title: Structure and expression of a cDNA encoding an RNA helicase-like protein in tobacco  
 A; Reference number: S42639; MUID:94154240; PMID:8111024  
 A; Accession: S42639  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-607 <ITR>  
 A; Cross-references: GB:D16247; NID:G466572; PIDN:BA003763.1; PID:9563986  
 C; Superfamily: tobacco ATP-dependent RNA helicase DB10; WW repeat homology  
 C; Keywords: ATP; nucleotide binding; P-loop  
 F; 18-56/Domain: WW repeat homology <WW1>  
 F; 189-196/Region: nucleotide-binding motif A (P-loop)  
 F; 294-299/Region: nucleotide-binding motif B  
 F; 298-301/Region: DEAD motif F  
 Query Match 38.9%; Score 45.5%; DB 1; Length 607;  
 Best Local Similarity 37.9%; Pred. No. 44;  
 Matches 11; Conservative 4; Mismatches 5; Indels 9; Gaps 1;  
 Qy 3 VEILIGRGRTECVLSN 22  
 Db 505 VKVLEGANGCVPTRLDNASRGGMGRAR 533

RESULT 13  
 D83406  
 Probable transmembrane sensor PA1911 [imported] - Pseudomonas aeruginosa (strain PAO1)  
 C; Species: Pseudomonas aeruginosa  
 C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 28-Jul-2003  
 C; Accession: D83406  
 R; Scovier, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Baldwin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Lory, S.; Olson, M.V.  
 Nature 416, 959-964, 2000  
 A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen  
 A; Reference number: A82950; MUID:10984043  
 A; Accession: D83406  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-316 <STO>  
 A; Cross-references: GB:AE004617; GB:AE004091; NID:g9947901; PIDN:AAGG5299.1; GSPDB:GN001  
 A; Experimental source: strain PAO1  
 C; Genetics:  
 A; Gene: PA1911  
 C; Superfamily: Fe2+-dicitrato sensor, transmembrane component

Query Match 38.5%; Score 45; DB 2; Length 316;  
 Best Local Similarity 54.5%; Pred. No. 27;  
 Matches 12; Conservative 12; Mismatches 6; Indels 2; Gaps 1;

Qy 2 RVEILLEGRTECVLNSNLRGRTY 23  
 Db 195 RVAVLAGRVE-LSPLHGRGRW 214

## RESULT 14

D70506 hypothetical protein Rv2733c - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C;Accession: D70506  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Radandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230  
 A;Accession: D70506  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-512 <COL>  
 A;Cross-references: GB:Z98209; GB:AU123456; NID:G3261838; PIDN:CAB10909.1; PID:9222967  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: Rv2733c  
 C;Superfamily: conserved hypothetical protein b0835

Query Match 38.5%; Score 45; DB 1; Length 512;  
 Best Local Similarity 42.3%; Pred. No. 44;  
 Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 1;  
 Qy 1 QRVEIL---EGRTECVLNSNLRGRTY 22  
 Db 408 QAEVLYATGEGRKDTVTARMGRAR 433

## RESULT 15

S22383 axonin 1 precursor - chicken  
 N;Alternate names: neural cell adhesion molecule AxCAM  
 C;Species: Gallus gallus (chicken)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C;Accession: S22383; S34107; S69332; S22128  
 R;Zueiliig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; C.  
 Bur. J. Biochem. 204, 453-463, 1992  
 A;Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immu  
 A;Reference number: S22383; MUID:92174898; PMID:1311675  
 A;Accession: S22383  
 A;Molecule type: DNA  
 A;Residues: 1-1036 <ZUE1>  
 A;Cross-references: EMBL:X63101; NID:g62852; PIDN:CMA44815.1; PID:962853  
 A;Accession: S34107  
 A;Molecule type: protein  
 A;Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;33  
 R;Giger, R.J.; Vogt, L.; Zueiliig, R.A.; Rader, C.; Henehan-Beatty, A.; Wolfer, D.P.; Sor  
 Bur. J. Biochem. 227, 617-628, 1995  
 A;Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.  
 A;Reference number: S69332; MUID:95172044; PMID:7867620  
 A;Accession: S69332  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1002-1036 <GIGs>  
 A;Cross-references: EMBL:X79607  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994  
 C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology  
 C;Keywords: cell adhesion  
 P;1-23/Domain: signal sequence #status predicted <SIG>  
 P;24-1036/Product: axonin 1 #status predicted <MAT>  
 P;3336-392/Domain: immunoglobulin homology <IMM>

Query Match 38.5%; Score 45; DB 2; Length 1036;

	Qy	Db	Best Local Matches	Local Similarity	Pred. No.	Gaps
	2 RVEILLEGRTECVLNSNLRGRTY 23	195 RVAVLAGRVE-LSPLHGRGRW 214	8	47.1%	2;	0;
			23	7 EGRTTECVLNSNLRGRTY		
			312	296 EGTYCEBAENIKGRDITY		

Search completed: MAY 6, 2004, 12:47:27  
 Job time : 22 secS

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Best Local Matches	Similarity 23;	Pred. No. 3.6e-11;	Indels 0;	Gaps 0;	DB XX	Human mature erythropoietin receptor EPOR extracellular domain #2.
Qy	1 QRVTELEGTECVLSNLRGRTRY 23				KW	Ligand; cell surface receptor; erythropoietin; EPOR; human;
Db	1 QRVTELEGTECVLSNLRGRTRY 23				KW	protein design automation; PDA.
					OS	Homo sapiens.
					XX	
					PN	WO20047612-A2.
					XX	
RESULT 4					PD 17-AUG-2000.	
ID AAR98938	standard; peptide; 30 AA.				XX 11-FEB-2000;	2000WO-US003665.
XX					XX	
AC AAR98938					PR 11-FEB-1999;	99US-0120009P.
XX					PR 29-APR-1999;	99US-0131674P.
DT 28-SEP-1996	(first entry)				XX	
XX	Synthetic human erythropoietin receptor peptide. SB-8.				PA (XENCOR INC.	
XX					XX	
KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;					PI Luo P, Dahiyaat B;	
KW erythropoiesis; erythrocyte production; epitope mapping.					XX	
XX					DR WPI; 2000-549135/50.	
OS Synthetic.					XX	
XX					PS Example 1; Fig 8; 82pp; English.	
PN WO9603448-A1.					XX	
XX					CC The present invention relates to a method for screening for a ligand	
PD 08-FEB-1996.					CC analog, comprising adding a candidate ligand to a non-naturally occurring	
XX					CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and	
PP 26-JUL-1995;	95WO-US009458.				CC determining the binding of the ligand to the analog. The present sequence	
XX					CC is a mature human erythropoietin receptor (EPOR) extracellular domain.	
PR 26-JUL-1994;	94US-00280864.				CC Protein Design Automation was carried out on the present sequence, so	
XX					CC that it may be used in the present invention as a cell surface receptor	
PA (AMGEN INC.					CC analog.	
XX					XX	
PI Elliott SG;					SQ Sequence 211 AA;	
XX					Query Match 100.0%; Score 117; DB 3;	
DR WPI; 1996-117004/12.					Best Local Similarity 100.0%; Pred. No. 4.7e-10;	
XX	Monoclonal antibodies stimulating an erythropoietin receptor - useful in				Matches 23; Conservative 0; Mismatches 0; Indels 0;	
PT diagnosis and treatment of patients having disorders associated with low					Gaps 0;	
PT red blood cell levels, e.g. anaemia.						
XX						
PS Example 6; Page 34; 61pp; English.						
XX					QY 1 QRVTELEGTECVLSNLRGRTRY 23	
AAR8960 R89965 and AAR8936-R98939 are overlapping, synthetic human					Db 161 QRVTELEGTECVLSNLRGRTRY 183	
CC erythropoietin receptor (shEPOR) peptides which span residues 1 to 244						
CC of the human EPOR. The peptides are used to map the EPOR binding epitope						
CC of an EPOR monoclonal antibody which binds to EPORs and stimulates						
CC erythropoiesis by stimulating the proliferation and/or differentiation of						
CC erythroid progenitor cells to erythrocytes. Pharmaceutical compsns.						
CC contng. the antibody may be used in the diagnosis and treatment of						
CC patients having disorders associated with low red blood cell levels, e.g.						
CC anaemia. The antibodies are also useful in methods and kits for detecting						
CC EPORs in biological samples						
XX Sequence 30 AA;						
SQ						
Query Match 100.0%; Score 117; DB 2;	Length 30;					
Best Local Matches 22;	Similarity Conservative 0;	Pred. No. 4.9e-11;	Indels 0;	Gaps 0;	DB XX	
Db					XX Ligand; cell surface receptor; erythropoietin; EPOR; human.	
					OS Homo sapiens.	
					XX PN WO20047612-A2.	
RESULT 5					PD 17-AUG-2000.	
AAB21686	standard; peptide; 211 AA.				XX 11-FEB-2000;	2000WO-US003665.
XX					XX	
AC AAB21686					PR 11-FEB-1999;	99US-0120009P.
XX					PR 29-APR-1999;	99US-0131674P.
DT 21-DEC-2000	(first entry)				XX PA (XENCOR INC.	
XX					XX	



194 OBVETII EGBTEMV. SNT. BGBTTBV. 216

Claim 1: SEO TD NO 48: AA722: English

PS Claim 1; SEQ ID NO 48; 447bp; English.

XX The invention relates to a novel isolated NOVX polypeptide. The  
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,  
 CC cardiotonic, hypotensive, antiarteriosclerotic, virucide, antibacterial,  
 CC fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,  
 CC anticonvulsant, osteopathic, antiarthritic antiinflammatory,  
 CC dermatological, antiasthmatic and antilipemic activities. The  
 CC polypeptides, nucleic acid molecules and antibodies may be useful for  
 CC treating or diagnosing diseases including metabolic disorders such as  
 CC diabetes and obesity, infectious diseases, anoxia, cancer,  
 CC cardiovascular diseases including hypertension and atherosclerosis,  
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic  
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.  
 CC Furthermore, the nucleic acids and polypeptides may also be used to  
 CC identify molecules that modulate or inhibit neurogenesis, cell  
 CC differentiation and proliferation, haemopoiesis, wound healing and  
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may  
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,  
 CC preventive medicine and pharmacogenomics. The current sequence is that of  
 CC the human NOV protein of the invention:  
 XX Sequence 458 AA;  
 SQ

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PS QRVELLEGRTECVLSNLQRGRTRY 216

XX BULT 9

ADBE28671 standard; protein: 458 AA.

ADBE28671;

29-JAN-2004 (first entry)

Human Nov15a protein - SEQ ID 48.

NOVX; antidiabetic; anorectic; cardiotonic; hypotensive;  
 antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;  
 nootropic; neuroprotective; antiparkinsonian; anticonvulsant;  
 osteopathic; antiarthritic; antiinflammatory; dermatological;  
 antiasthmatic; antilipemic; metabolic; diabetes; obesity; infectious;  
 anorexia; cancer; cardiovascular; hypertension; atherosclerosis;  
 neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;  
 osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;  
 neurogenesis; cell differentiation; proliferation; haemopoiesis;  
 wound healing; human; gene therapy; chromosome mapping;  
 tissue typing; human; NOV.

3

```

Homo sapiens.
WO2003040330-A2.
15-MAY-2003.
05-NOV-2002; 2002WO-US035536.
05-NOV-2003; 2003US05556720

Query Match          100.0%; Score 117; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.e-09;
Matches 23; Conservatve 0; Mismatches 0;
Indels 0; Gaps 0
Qy      1 QRVEELGRTECVLSNLGRTRY 213
Db      194 QRVEELGRTECVLSNLGRTRY 216

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03-NOV-2001 : 2001US-0338828E.  
05-DEC-2001 : 2001US-0336600B

BESTILLT 10

ADE22673	ID	ADE22673	standard; protein;	458 AA.
XX				
AC	AC	ADE22673,		
XX				
DT	29-JAN-2004	(first entry)		
XX				
DB		Human NOV15b protein - SBQ ID 50.		
XX				
KW		NOVX; antidiabetic; anorectic; cardiotonic; hypotensive;		
KW		antirheumatic; viricide; antibiotic; fungicide; protozoacide;		
KW		neuroprotective; antibacterial; anticonvulsant;		
KW		nootropic; neuroprotective; anti-parkinsonian; dermatological;		
KW		osteopathic; antiarthritic; anti-inflammatory; metabolic; diabetes; obesity; infectious;		
KW		antiasthmatic; anti-platelet; hypertension; atherosclerosis;		
KW		anoxia; cancer; cardiovascular; hypertension; Alzheimer's disease; Parkinson's; epilepsy; immune;		
KW		neurodegenerative; haemopoietic; inflammatory skin; dyslipidaemia;		
KW		osteoarthritis; cell differentiation; proliferation; haemopoiesis;		
KW		neurogenesis; angiogenesis; gene therapy; chromosome mapping;		
KW		wound healing; human; NOV.		
KW		tissue typing;		
KW				

PR	17-APR-2002;	2002US-0373288P.	DB	Human NOV15c protein - SEQ ID 52.		
PR	15-MAY-2002;	2002US-0380981P.	XX			
PR	17-MAY-2002;	2002US-0381491P.	KW	NOVX; antidiabetic; anorectic; cardioton; fungicide; protozoacide;		
PR	28-MAY-2002;	2002US-0383534P.	KW	antiarteriosclerotic; viricide; antibacterial; fungicide; anticonvulsant;		
PR	28-MAY-2002;	2002US-0383744P.	KW	nootropic; neuroprotective; antiparkinsonian; antidermatological;		
PR	29-MAY-2002;	2002US-0384024P.	KW	osteopathic; antiarthritic; antiinflammatory;		
PR	29-MAY-2002;	2002US-0384024P.	KW	antiasthmatic; antilipaemic; metabolic; diabetes; obesity; infectious;		
PR	07-AUG-2002;	2002US-0401788P.	KW	anorexia; cancer; cardiovascular; hypertension; atherosclerosis;		
PR	26-AUG-2002;	2002US-0406353P.	KW	neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;		
PR	31-OCT-2002;	2002US-00287971.	KW	osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;		
XX	(CURA-)	CURAGEN CORP.	KW	neurogenesis; cell differentiation; proliferation; haemopoiesis;		
XX			KW	wound healing; angiogenesis; gene therapy; chromosome mapping;		
XX			KW	tissue typing; human; NOV.		
PI	Alsobrook JP,	Alvarez E,	Baron M,	Boldog FL;	XX	
PI	Ellerman K,	Casman SU,	Dhanabai A,	Edinger SR,	OS	
PI	Grosse WM,	Ettenberg S,	Gangolli EA,	Gerlach VI,	XX	
PI	Guo X,	Hackett C,	Ji W,	Gorman L;	WO2003040330-A2.	
PI	Lepley DM,	Li L,	Kekuda R,	Khrantsov NV;	PN	
PI	Mezes PS,	Macdougall JR,	Malyankar UM,	Mcqueeney K;	XX	
PI	Pena CEA,	Millet I,	Mishra VS,	Padigaru M,	PD	15-MAY-2003.
PI	Peyman JA,	Raselli L,	Rieger DK,	Shenoy SG,	XX	
PI	Schroder G,	Szczerba KA,	Stone DJ,	Shimkets RA;	PP	05-NOV-2002;
PI	Vernet CAM,	Zerhusen BD,	Zhong M;	Tchernev VT,	XX	2002WO-US035536.
XX	WPI;	2003-411555/41.	XX	XX	2002US-0338626P.	
DR	N-PSDB;	ADB28672.	XX	PR	2001US-0338600P.	
XX			PR	PR	05-DEC-2001;	
PT	New isolated NOVX polypeptides and polynucleotides, useful for	PR	PR	07-DEC-2001;	2001US-033885P.	
PT	preventing, diagnosing or treating NOVX-associated disorders, e.g.	PR	PR	12-DEC-2001;	2001US-0341346P.	
PT	osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,	PR	PR	17-DEC-2001;	2001US-0341477P.	
PT	or infections.	PR	PR	17-DEC-2001;	2001US-0341540P.	
XX	Claim 1; SEQ ID NO 50; 447PP; English.	PR	PR	20-DEC-2001;	2001US-0342592P.	
PS	The invention relates to a novel isolated NOVX polypeptide. The	PR	PR	27-DEC-2001;	2001US-0344197P.	
CC	polypeptide of the invention demonstrates, antiarteritic, anorectic,	PR	PR	31-DEC-2001;	2001US-0344903P.	
CC	cardioton, hypotensive, antiarteriosclerotic, viricide, antibacterial,	PR	PR	17-APR-2002;	2002US-037388P.	
CC	fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,	PR	PR	17-MAY-2002;	2002US-0380981P.	
CC	anticonvulsant, osteoprotective, antiarthritic, antiinflammatory,	PR	PR	17-MAY-2002;	2002US-0381491P.	
CC	dermatoactive, antiasthmatic and antiinflammatory. The	PR	PR	28-MAY-2002;	2002US-0383534P.	
CC	polypeptides, nucleic acid molecules and antibodies may be useful for	PR	PR	29-MAY-2002;	2002US-0383744P.	
CC	treating or diagnosing diseases including metabolic disorders such as	PR	PR	07-AUG-2002;	2002US-0384024P.	
CC	diabetes and obesity, infectious diseases, anorexia, cancer,	PR	PR	26-AUG-2002;	2002US-0406535P.	
CC	cardiovascular diseases including hypertension and atherosclerosis,	PR	PR	31-OCT-2002;	2002US-00287971.	
CC	neurodegenerative disorders such as Alzheimer's disease, Parkinson's	PA	(CURA-)	CURAGEN CORP.		
CC	disease and epilipsy, immune disorders e.g. osteoarthritis, haemopoietic	XX				
CC	disorders, inflammatory skin disorders, asthma and dyslipidaemia.	XX				
CC	Furthermore, the nucleic acids and polypeptides may also be used to	XX				
CC	identify molecules that modulate or inhibit neurogenesis, cell	XX				
CC	differentiation and proliferation, haemopoiesis, wound healing and	XX				
CC	angiogenesis, as well as in gene therapy. Finally, the nucleic acids may	XX				
CC	be used as hybridisation probes in chromosome mapping, tissue typing,	XX				
CC	preventive medicine and pharmacogenomics. The current sequence is that of	XX				
CC	the human NOV protein of the invention.	XX				
SQ	Sequence 458 AA;	XX				
Query Match	100.0%;	Score 117;	DB 7;	Length 458;	XX	
Best Local Similarity	100.0%;	Pred. No. 1.1e-09;			XX	
Matches	0;	Mismatches 0;	Indels 0;	Gaps 0;	PT	
Qy	1 ORVBILBERTECTYLSNURGTRY 23				PT	
Db	194	ORVBILBERTECTYLSNURGTRY 216			PT	
RESULT	11				PT	
ADE28675					CC	
ID	ADE28675	standard; protein: 458 AA.			CC	
XX	AC				CC	
XX	DT				CC	
DT	29-JAN-2004	(First entry)			CC	

cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorder, inflammatory skin disorders, asthma and dyslipidaemia. Furthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopoiesis, wound healing and angiogenesis, as well as gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.

Sequence 458 AA;

Query Match	100.0%	Score 117;	DB 7;	Length 458;
Best Local Similarity	100.0%	Pred. No. 1.1e-09;		
Matches	23;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;		

Qy 1 QRVELLEGRTCECVLSNLRGTRY 23  
Db 194 QRVELLEGRTCECVLSNLRGTRY 216

RESULT 12  
ID AAW08349 standard; protein; 488 AA.  
XX  
AC AAW08349;  
XX DT 14-MAR-1997 (first entry)  
XX DE EpoR<sup>C</sup> Fusion protein.  
XX KW Receptor agonist; antibody; erythropoietin receptor; EpoR; immunogen; antigen; metallothionein; promoter; IgG1; Fc; anaemia; therapy.  
XX OS Homo; sapiens.  
XX OS Synthetic.  
XX OS Chimeric.  
XX Key Location/Qualifiers  
PT 1. ^250  
PT /label= EpoR-ECDF  
PT /note= "erythropoietin receptor extracellular domain"  
PT Cleavage-site 251. .254  
PT Note= "Factor Xa cleavage site"  
PT Domain 255. .488  
PT /label= Fc  
PT /note= "human IgG1 Fc sequence"  
XX WO964021-A1.  
PN 19-DEC-1996.  
XX 07-JUN-1996; 96WO-US009613.  
XX 07-JUN-1995; 95US-00474673.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Young PR; Erickson-Miller CL;  
XX WPI; 1997-051900/05.  
DR N-PSDB; RAT48800.  
XX Recombinant immunogen correspond to dimeric form of a receptor - used for generating antibodies able to act as receptor agonists, esp. of erythropoietin receptor for treating anaemia.  
XX Example 1; Page 39-41; 83pp; English.

A fusion protein (AAW08349) encoded by plasmid ntaEpoR<sup>C</sup> (AAW48800), comprises the human erythropoietin receptor (Epo<sup>R</sup>) extracellular domain

CC fused (via a Factor Xa cleavage sequence) to the Fc portion of human IgG1. It can be expressed e.g. in transfected Drosophila S2 cells upon induction with copper sulphate. The cells secrete EpoR<sup>C</sup> as a dimeric molecule due to the affinity of the Fc moiety for itself. The dimeric receptor can be used as an immunogen to generate antibodies (monoclonal, polyclonal, chimeric, humanised) able to act as Epo<sup>R</sup> agonists for use in treatment of anaemia  
XX Sequence 488 AA;

Query Match	100.0%	Score 117;	DB 2;	Length 488;
Best Local Similarity	100.0%	Pred. No. 1.2e-09;		
Matches	23;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;		

Qy 1 QRVELLEGRTCECVLSNLRGTRY 23  
Db 194 QRVELLEGRTCECVLSNLRGTRY 216

RESULT 13  
ID AAB13012 standard; protein; 503 AA.  
XX  
AC AAB13012;  
XX DT 08-DEC-2000 (first entry)  
XX DB Q-tagged erythropoietin (EPO) receptor protein.  
XX KW Site specific label; detection; interaction screening; transglutaminase; erythropoietin receptor; EPO.  
XX OS Synthetic.  
XX WO200043492-A2.  
PN 2000WO-US001481.  
XX PD 27-JUL-2000.  
XX PP 20-JAN-2000; 2000WO-US001481.  
XX PR 22-JAN-1999; 99US-0117327P.  
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX PI Tew DG, Powell DJ, Meek TD, Chen W;  
XX DR WPI; 2000-49922/44.  
XX PT Screening for a candidate compound for use in bioassays comprises contacting the candidate molecule with a labelled modified protein and detecting the label to identify interaction of the two molecules.  
PT Example 4; Page 26; 49pp; English.  
XX PS This invention relates to methods for the site specific modification of a protein, and to a method for screening for a candidate compound which interacts with first protein. The screening method comprises contacting the candidate molecule with a labelled modified first protein and detecting the label to identify interaction of the labelled modified first protein and candidate compound. The first protein is modified to contain a peptide, represented by sequence ABI3005. The method is used to label proteins at specific sites. The present sequence represents a Q-tagged erythropoietin (EPO) receptor constructed in an example of the method of the invention  
XX Sequence 503 AA;

Query Match	100.0%	Score 117;	DB 3;	Length 503;
Best Local Similarity	100.0%	Pred. No. 1.3e-09;		
Matches	23;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;		

Qy 1 QRVELLEGRTCECVLSNLRGTRY 23  
Db 194 QRVELLEGRTCECVLSNLRGTRY 216

Db	194	QRVLEILGRTECVLSNLRGRTRY 216	XX	Homo sapiens.
RESULT 14			OS	
AAR6512			XX	
ID AAR6512	standard; protein; 508 AA.		Key	Location/Qualifiers
XX			FT	1. .24
AAR6512;			Peptide	/note= "signal peptide"
AC			FT	25. .508
XX	25-MAR-2003 (revised)		Protein	/note= "mature EPO receptor"
DT	04-JAN-1991 (First entry)		FT	251. .272
DE	EPO receptor.		Region	/note= "putative transmembrane domain"
XX			FT	
KW	Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.		FT	
XX			PN	US5278065-A.
OS	Homo sapiens.		XX	
XX			PD	11-JAN-1994.
PN	WO9008822-A.		XX	
XX			PF	25-MAR-1991;
PD	09-AUG-1990.		XX	91US-00678877.
XX			PR	03-FEB-1989;
PP	03-FEB-1989;	89US-00306503.	XX	89US-00306503.
XX			PA	(GEMY ) GENETICS INST INC.
PR	03-FEB-1989;	89US-00306503.	XX	(CHIL ) CHILDRENS MEDICAL CTR.
XX			PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES.
D'andrea A,	Wong GG,	Jones SS;	PI	
XX			XX	
WPI:	1994-025409/03.		DR	
PA	(GEMY ) GENETICS INST INC.		N-PSDB; AAQ53395.	
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES.		XX	
Dandrea A,	Wong G;		PT	Recombinant DNA encoding erythropoietin receptor - used to develop prods.
XX			PT	for study, treatment or diagnosis of disorders in which receptor is dysfunctional.
DR	1990-260931/34.		PT	
XX			XX	Disclosure: Fig 9; 24PP; English.
PT	Erythropoietin receptor and gene - used for developing reagents and		XX	
PT	systems to control and study erythropoiesis.		CC	Mouse erychroleukaemia (MEL) cells were used to construct a cDNA library.
XX			CC	The cDNA was used to transfet COS-1 cells and these were screened for
PS	radiiodinated erythropoietin (EPO) binding to isolate cDNA encoding the		CC	EPO receptor. This cDNA was used as a probe to screen a human genomic
PS	sequence to obtain DNA encoding the human EPO receptor. The cDNA may		CC	be used to study, treat or diagnose disorders in which the EPO receptor
PS	is dysfunctional. The EPO receptor may also be used to raise antibodies or		CC	for treating hypersensitivity to EPO or who have elevated levels of EPO.
PS	CC		CC	The prod is pref. used for treating anaemias, primary proliferative
PS	CC		CC	polycythemia and secondary polycythemia. See also AAR17517. (Updated on
PS	CC		CC	25-MAR-2003 to correct PP field.)
PS	CC		XX	Sequence 508 AA;
PS	CC		XX	Query Match 100.0%; Score 117; DB 2; Length 508;
PS	CC		XX	Best Local Similarity 100.0%; Pred. No. 1.3e-09; Mismatches 0; Indels 0; Gaps 0;
PS	CC		XX	Matches 23; Conservative 0;
PS	CC		Qy 1 ORVLEILGRTECVLSNLRGRTRY 23	
PS	CC		Db 194 ORVLEILGRTECVLSNLRGRTRY 216	
PS	CC		Search completed: May 6, 2004, 12:45:02	
PS	CC		Job time : 55 SECs	
RESULT 15				
AAR47518				
ID AAR47518	standard; protein; 508 AA.			
XX				
AC AAR47518;				
XX				
DT 25-MAR-2003 (revised)				
DT 24-JUN-1994 (First entry)				
XX				
DE Human EPO receptor.				
XX				
KW Erythropoietin receptor; recombinant; murine; anaemia.				

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	Sequence 2, Appli			
Run on:	May 6, 2004, 12:42:22 ; Search time 23 Seconds (without alignments)	Sequence 14, Appli			
Title:	US-10-612-885A-1	Sequence 6212, Appli			
Perfect score:	117	Sequence 14, Appli			
Sequence:	1 QRVBLIGRTECVLSNLGRTRY 23	Sequence 15, Appli			
Scoring table:	BLOSUM62	Sequence 13, Appli			
Gapext:	0.5	Sequence 438, Appli			
Searched:	389414 seqs, 51625971 residues	Sequence 3535, Appli			
Total number of hits satisfying chosen parameters:	389414	Sequence 17331, Appli			
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Maximum DB seq length: 2000000000		Sequence 243, Appli			
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	Maximum Match 100%	Sequence 20894, Appli			
	Listing first 45 summaries	Sequence 6, Appli			
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	3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*	Sequence 6, Appli			
	4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*	Sequence 6, Appli			
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	6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*	Sequence 6, Appli			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
		SUMMARIES			
Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	23	4 US-09-028-937-11	Sequence 11, Appli
2	117	100.0	30	2 US-08-280-864A-12	Sequence 12, Appli
3	117	100.0	30	4 US-09-032-291-12	Sequence 12, Appli
4	117	100.0	438	4 US-09-339-838-5	Sequence 5, Appli
5	117	100.0	438	4 US-09-339-838-7	Sequence 7, Appli
6	117	100.0	488	3 US-08-776-511-2	Sequence 2, Appli
7	117	100.0	508	2 US-09-850-293-5	Sequence 5, Appli
8	49	41.9	321	3 US-09-039-609-4	Sequence 4, Appli
9	49	41.9	458	3 US-09-039-609-2	Sequence 2, Appli
10	46	39.3	64	4 US-09-13-000C-5287	Sequence 2, Appli
11	46	39.3	67	4 US-09-732-210-1599	Sequence 159, Appli
12	45	39.3	67	4 US-09-732-210-1600	Sequence 160, Appli
13	45	38.5	372	4 US-09-489-039A-12903	Sequence 32067, Appli
14	44	37.6	493	4 US-09-134-000C-3764	Sequence 12903, Appli
15	43	36.8	931	4 US-08-524-655A-2	Sequence 2, Appli
16	42	35.9	67	4 US-09-732-210-101	Sequence 1601, Appli
17	42	35.9	252	4 US-09-232-994A-3222	Sequence 3222, Appli
18	42	35.9	283	4 US-08-956-171B-5203	Sequence 5203, Appli
19	42	35.9	363	4 US-09-134-000C-3764	Sequence 3764, Appli
20	42	35.9	605	2 US-08-572-307B-8	Sequence 8, Appli
21	42	35.9	605	4 US-09-070-802-8	Sequence 8, Appli
22	42	35.9	605	4 US-09-991-326-8	Sequence 8, Appli
23	42	35.9	623	1 US-08-232-994A-2393	Sequence 23930, Appli
24	42	35.9	1018	1 US-08-452-052-2	Sequence 2, Appli
25	42	35.9	1101	3 US-08-386-483-5	Sequence 6, Appli
26	42	35.9	1611	2 US-08-804-227C-4	Sequence 5, Appli
27	42	35.9	3729	2 US-08-804-227C-11	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-09-028-937-11  
; Sequence 11, Application US/09028937  
; Patent No. 63133031  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Lemnart  
; TITLE OF INVENTION: Receptor Derived Peptides As Modulators  
; NUMBER OF INVENTION: Of Receptor Activity  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/028, 937  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/788, 820  
; FILING DATE: 23-JAN-1997  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/701, 182  
; FILING DATE: 22-AUG-1996  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/612, 999  
; FILING DATE: 08-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silva, Robin M.  
; TELEFAX: (415) 949-8111  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-09-028-937-11

Query Match 100.0%; Score 117; DB 4; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;

Qy 1 ORVIELLEGRTECVLSNLRGTRY 23  
 Db 1 ORVIELLEGRTECVLSNLRGTRY 23

---

RESULT 2  
 US-08-280-864A-12  
 ; Sequence 12, Application US/08280864A

GENERAL INFORMATION:  
 APPLICANT: Elliott, Steven G.  
 TITLE OF INVENTION: Antibodies Which Activate an  
 TITLE OF INVENTION: Erythorpoietin Receptor  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
 STREET: 1840 De havilland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 91320  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/280, 864A  
 FILING DATE:  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE DOCKET NUMBER: A-307  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein

US-08-280-864A-12

Query Match 100.0%; Score 117; DB 2; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;

Qy 1 ORVIELLEGRTECVLSNLRGTRY 23  
 Db 1 ORVIELLEGRTECVLSNLRGTRY 23

RESULT 3  
 US-09-092-291-12  
 ; Sequence 12, Application US/09092291  
 ; Patent No. 6319499  
 GENERAL INFORMATION:  
 APPLICANT: Elliott, Steven G.  
 TITLE OF INVENTION: Antibodies Which Activate an  
 TITLE OF INVENTION: Erythorpoietin Receptor  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.

STREET: One Amgen Center Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 91320  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/092,291  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/280864

FILING DATE: 25-JUL-1994  
 ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-307A

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;

RESULT 4  
 US-09-339-838-5  
 ; Sequence 5, Application US/09339838

GENERAL INFORMATION:

NAME: Bell, David N.

REFERENCE/DOCKET NUMBER: Bell, David N.

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-339-838-5

Query Match 100.0%; Score 117; DB 4; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;

RESULT 5  
 US-09-339-838-7  
 ; Sequence 7, Application US/09339838

GENERAL INFORMATION:

NAME: Mueller, Susan G.

REFERENCE/DOCKET NUMBER: Mueller, Susan G.

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-339-838-7

Query Match 100.0%; Score 117; DB 4; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;

RESULT 6  
 US-09-339-838-23  
 ; Sequence 23, Application US/09339838

GENERAL INFORMATION:

NAME: Matthews, Kathryn E.

REFERENCE/DOCKET NUMBER: Matthews, Kathryn E.

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-339-838-23

Query Match 100.0%; Score 117; DB 4; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-12; Indels 0; Gaps 0;

TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglo  
FILE REFERENCE: 6704-93  
CURRENT APPLICATION NUMBER: US/09/339,838  
CURRENT FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: CA 2,260,332  
PRIOR FILING DATE: 1999-01-25  
PRIOR APPLICATION NUMBER: CA 2,241,576  
PRIOR FILING DATE: 1998-06-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-339-838-7

Length: 438

Query Match 100.0%; Score 117; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 4.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLELGRTECVLSNLQRTRY 216  
Db 194 QRVLELGRTECVLSNLQRTRY 216

RESULT 6  
US-08-776-511-2 Application US/08776311  
Patent No. 6153190  
GENERAL INFORMATION:  
APPLICANT: Young, Peter R.  
APPLICANT: Brickson-Miller, Connie  
TITLE OF INVENTION: Method for Obtaining Receptor Agonist  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation- Corporate  
STREET: 709 Sweden Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,511  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervis, Herbert H.  
REGISTRATION NUMBER: 31,171  
REFERENCE/DOCKET NUMBER: SBC P50349-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5015  
TELEFAX: 610-270-5090  
INFORMATION FOR SBQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-776-511-2

Query Match 100.0%; Score 117; DB 3; Length 488;  
Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLELGRTECVLSNLQRTRY 23  
Db 194 QRVLELGRTECVLSNLQRTRY 216

RESULT 8  
US-09-339-609-4  
Sequence 4, Application US/09039609  
Patent No. 6107473  
GENERAL INFORMATION:  
APPLICANT: KIRKLY, KRISTINE  
TITLE OF INVENTION: A KRINGLES-RELATED CLONE,  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA

COUNTRY: USA  
 ZIP: 19482  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FasSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/039,609  
 FILING DATE: 16-MAR-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/060,623  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestia, Paul F.  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GP-70275  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-407-0700  
 TELEFAX: 610-407-0701  
 TELEX:  
 QUERY FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 321 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-09-039-609-4

Query Match 41.9%; Score 49; DB 3; Length 321;  
 Best Local Similarity 50.0%; Pred. No. 4.1%;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VELIEGRTECVLSNLGRTR 22  
 Db 226 VELUDGYTHRVLARFRGGSR 245

RESULT 9  
 US-09-039-609-2  
 Sequence 2, Application US/09039609  
 GENERAL INFORMATION:  
 APPLICANT: ALBONE, EARL  
 APPLICANT: KIKLY, KRISTINE  
 TITLE OF INVENTION: A KRINGLE-RELATED CLONE,  
 TITLE OF INVENTION: HTHBZ47  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rainer & Prestia  
 STREET: P.O. Box 980  
 CITY: Valley Forge  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19482  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FasSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/039,609  
 FILING DATE: 16-MAR-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/060,623  
 FILING DATE: 01-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestia, Paul F.  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GP-70275

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-407-0700  
 TELEFAX: 610-407-0701  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 458 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-039-609-2

Query Match 41.9%; Score 49; DB 3; Length 458;  
 Best Local Similarity 50.0%; Pred. No. 6.3%;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VEILEGRTECVLSNLGRTR 22  
 Db 270 VELUDGYTHRVLARFRGGSR 289

RESULT 10  
 US-09-134-000C-5287  
 Sequence 5287, Application US/09134000C  
 GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 0327956-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 PRIORITY NUMBER: US 60/055,778  
 PRIORITY FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 5287  
 LENGTH: 64  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-5287

Query Match 39.3%; Score 46; DB 4; Length 64;  
 Best Local Similarity 60.0%; Pred. No. 1.9%;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VEILEGRTECVLSNLGRTR 17  
 Db 11 VELIEGRTECVLSNLGRTR 25

RESULT 11  
 US-09-732-210-1599  
 Sequence 1599, Application US/097322210  
 GENERAL INFORMATION:  
 APPLICANT: Bunkers, Greg J.  
 APPLICANT: Liang, Jihong  
 APPLICANT: Mittanck, Cindy A.  
 APPLICANT: Seale, Jeffrey W.  
 APPLICANT: Wu, Yonnie S.  
 TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
 FILE REFERENCE: 38-21(15036)B  
 CURRENT APPLICATION NUMBER: US/09/732,210  
 PRIORITY NUMBER: US 60/169,513  
 PRIORITY FILING DATE: 2000-12-07  
 PRIORITY NUMBER: US 60/169,513  
 PRIORITY FILING DATE: 1999-12-07  
 PRIORITY NUMBER: US 60/169,340  
 NUMBER OF SEQ ID NOS: 1753  
 SEQ ID NO 1599  
 LENGTH: 67

Qy 2 RVEILEGRTECVLSNLRGRTY 23  
; ORGANISM: Kluyveromyces lactis  
US-09-732-2101599

Query Match 39.3%; Score 46; DB 4; Length 67;  
Best Local Similarity 42.9%; Pred. No. 2;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 29 RVEILEGRTECVLSNLRGRT 22  
29 RVBFLEDTRTIVRNVKGPVR 49

RESULT 12  
US-09-732-2101600  
Sequence 1600, Application US/09732210  
Patent No. 6573161  
GENERAL INFORMATION:  
APPLICANT: Bunkers, Greg J.  
APPLICANT: Liang, Jihong  
APPLICANT: Mittanck, Cindy A.  
APPLICANT: Seale, Jeffrey W.  
APPLICANT: Wu, Yonnie S.  
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
FILE REFERENCE: 38-21(15036)B  
CURRENT APPLICATION NUMBER: US/09/32,210  
PRIORITY FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: US 60/169,513  
PRIORITY FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: US 60/169,340  
PRIORITY FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 1753  
SEQ ID NO: 1600  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Kluyveromyces marxianus  
US-09-732-2101600

Query Match 39.3%; Score 46; DB 4; Length 67;  
Best Local Similarity 42.9%; Pred. No. 2;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 29 RVEILEGRTECVLSNLRGRT 22  
29 RVBFLEDTRTIVRNVKGPVR 49

RESULT 13  
US-09-252-991A-32067  
Sequence 32067, Application US/09252991A  
Patent No. 6551195  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
CURRENT APPLICATION NUMBER: US/09/252,991A  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
SEQ ID NO: 32067  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Psuedomonas aeruginosa  
US-09-252-991A-32067

Query Match 38.5%; Score 45; DB 4; Length 372;  
Best Local Similarity 54.5%; Pred. No. 22;  
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 2 RVEILEGRTECVLSNLRGRTY 23  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12903  
SEQ ID NO: 1903  
LENGTH: 493  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12903

RESULT 14  
US-09-489-039A-12903  
Sequence 12903, Application US/09489039A  
Patent No. 6610636  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al.  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004.001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO: 1903  
LENGTH: 493  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12903

Query Match 37.6%; Score 44; DB 4; Length 493;  
Best Local Similarity 45.0%; Pred. No. 45;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 4 EILEGRTECVLSNLRGRTY 23  
; ORGANISM: Actinobacillus pleuropneumoniae  
Db 111 EALEGKTPCVRVRRGRHEP 130

RESULT 15  
US-08-624-655A-2  
Sequence 2, Application US/08624655A  
GENERAL INFORMATION:  
APPLICANT: DABAN, MONTSERRAT  
APPLICANT: MEDRANO, ANDRES  
APPLICANT: ESPUNA, ENRIC  
APPLICANT: QUEROL, ENRIQUE  
APPLICANT: QUEIROZ, MARINA  
TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (TBP1) GENE OF  
TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE, ITS USE TO PREPARE  
TITLE OF INVENTION: PRODUCTS FOR THE UTILIZATION IN VACCINES FOR  
TITLE OF INVENTION: PLEUROPNEUMONIA AND AS DIAGNOSTIC REAGENTS  
FILE REFERENCE: P00740  
CURRENT APPLICATION NUMBER: US/08/624,655A  
CURRENT FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: 95 00592  
PRIOR FILING DATE: 1995-03-24  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 2  
LENGTH: 931  
TYPE: PRT  
ORGANISM: Actinobacillus pleuropneumoniae  
US-08-624-655A-2

Query Match 36.8%; Score 43; DB 4; Length 931;  
Best Local Similarity 33.3%; Pred. No. 1.4e+02;  
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 6 LEGRTECVLSNLRGRTY 23  
; ORGANISM: Actinobacillus pleuropneumoniae  
Db 581 IAGRADCATSKIKSHNY 598.

Search completed: May 6, 2004, 12:46:53  
Job time : 23 SECs



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OM protein - protein search, using SW mode!

Run on: May 6, 2004, 12:45:07 ; Search time 42 Seconds

(without alignments)  
 152.001 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLELEGTECVLSNLGRTRY 23

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA.\*

1: /cgn2\_6\_ptodata/1/pubpa/us07\_PUBCOMB.pep;\*  
 2: /cgn2\_6\_ptodata/1/pubpa/us06\_PUBCOMB.pep;\*  
 3: /cgn2\_6\_ptodata/1/pubpa/us07\_NEW\_PUB.pep;\*  
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 10: /cgn2\_6\_ptodata/1/pubpa/us09\_E\_PUBCOMB.pep;\*  
 11: /cgn2\_6\_ptodata/1/pubpa/us09\_E\_PUBCOMB.pep;\*  
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 18: /cgn2\_6\_ptodata/1/pubpa/us60\_PUBCOMB.pep;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match ID	Length	DB ID	Description
1	11.7	100.0	23	9 US-09-991-548-11	Sequence 11, Appl
2	11.7	100.0	23	16 US-10-231-494-30	Sequence 30, Appl
3	11.7	100.0	30	15 US-10-364-276-12	Sequence 12, Appl
4	11.7	100.0	458	12 US-10-287-971-50	Sequence 46, Appl
5	11.7	100.0	458	12 US-10-287-971-52	Sequence 50, Appl
6	11.7	100.0	458	12 US-10-287-971-52	Sequence 52, Appl
7	11.7	100.0	508	9 US-09-016-159-5	Sequence 5, Appl
8	11.3	96.6	508	12 US-10-287-971-54	Sequence 54, Appl
9	10.3	88.0	109	15 US-10-316-194-142	Sequence 142, App
10	10.3	82.1	109	15 US-10-316-194-144	Sequence 144, App
11	9.3	79.5	109	15 US-10-316-194-35	Sequence 35, Appl
12	8.6	73.5	109	15 US-10-316-194-43	Sequence 43, Appl
13	5.2	44.4	1026	10 US-09-947-063-4	Sequence 4, Appl
14	5.2	44.4	1026	10 US-09-947-063-11	Sequence 11, Appl
15	4.9	41.9	49	9 US-09-728-912-7	Sequence 7, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match ID	Length	DB ID	Description
1	11.0	41.9	373	13 US-10-042-431-6	Sequence 27439, A
2	11.0	41.9	373	10 US-09-759-130B-376	Sequence 4, Appl
3	11.0	41.9	413	9 US-09-728-912-2	Sequence 6, Appl
4	11.0	41.9	413	10 US-09-759-130B-413	Sequence 2, Appl
5	11.0	41.9	451	13 US-10-042-431-43	Sequence 43, Appl
6	11.0	41.9	456	13 US-10-042-431-5	Sequence 375, Appl
7	11.0	41.9	458	16 US-10-047-042-16	Sequence 5, Appl
8	11.0	41.9	470	13 US-10-042-431-6	Sequence 439, Appl
9	11.0	41.9	475	10 US-09-759-130B-373	Sequence 69, Appl
10	11.0	41.9	475	10 US-10-042-431-52	Sequence 3, Appl
11	11.0	41.9	492	15 US-10-034-749-2546	Sequence 2546, Appl
12	11.0	41.0	312	9 US-09-738-626-5282	Sequence 5282, Appl
13	11.0	41.0	312	9 US-10-349-493-9725	Sequence 9725, Appl
14	11.0	40.6	419	15 US-10-059-386-32900	Sequence 3200, A
15	11.0	40.2	85	14 US-10-042-431-48	Sequence 181458,
16	11.0	40.2	191	12 US-10-042-459-181458	Sequence 50, Appl
17	11.0	40.2	386	12 US-10-042-459-18157	Sequence 181457,
18	11.0	39.3	494	12 US-10-042-114-50005	Sequence 50005, A
19	11.0	39.3	941	12 US-10-042-114-72012	Sequence 72012, A
20	11.0	38.5	686	15 US-10-162-335-46	Sequence 46, Appl
21	11.0	38.5	686	15 US-10-162-335-48	Sequence 48, Appl
22	11.0	38.5	686	15 US-10-162-335-50	Sequence 50, Appl
23	11.0	38.5	686	15 US-10-162-335-52	Sequence 52, Appl
24	11.0	38.5	961	12 US-10-042-433-42	Sequence 42, Appl
25	11.0	37.6	87	12 US-10-042-459-196538	Sequence 196538,
26	11.0	37.6	250	12 US-10-042-599-236053	Sequence 236053,
27	11.0	37.6	873	12 US-10-0425-114-65968	Sequence 65968, A

#### ALIGNMENTS

RESULT 1	US-09-991-548-11	; Sequence 11, Application US/09991548.
		; Patent No. US2002016013A1
		; GENERAL INFORMATION:
		; APPLICANT: OLSSON, Lennart
		; INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS
		; TITLE OF INVENTION: RECEPTOR ACTIVITY
		; FILE REFERENCE: 215420000101
		; CURRENT APPLICATION NUMBER: US/09/991,548
		; CURRENT FILING DATE: 2001-11-20
		; PRIOR APPLICATION NUMBER: 09/028,937
		; PRIOR FILING DATE: 1998-02-24
		; PRIOR APPLICATION NUMBER: 08/788,820
		; PRIOR FILING DATE: 1997-01-23
		; PRIOR APPLICATION NUMBER: 08/701,382
		; PRIOR FILING DATE: 1996-08-22
		; PRIOR APPLICATION NUMBER: 08/612,999
		; NUMBER OF SEQ ID NOS: 44
		; SOFTWARE: FastSeq for Windows Version 4.0
		; SEQ ID NO 11
		; LENGTH: 23
		; TYPE: PRT
		; ORGANISM: Artificial Sequence
		; FEATURE:
		; OTHER INFORMATION: human erythropoletin receptor
		US-09-991-548-11

Query Match ID	Score	Length	DB ID	Description
1	100.0	23	9 US-09-991-548-11	Sequence 11, Appl
2	100.0	16	US-10-231-494-30	Sequence 30, Appl
3	100.0	15	US-10-364-276-12	Sequence 12, Appl
4	100.0	12	US-10-287-971-50	Sequence 46, Appl
5	100.0	12	US-10-287-971-52	Sequence 50, Appl
6	100.0	9	US-09-016-159-5	Sequence 5, Appl
7	100.0	9	US-09-016-159-5	Sequence 54, Appl
8	96.6	508	12 US-10-287-971-54	Sequence 142, App
9	88.0	109	15 US-10-316-194-142	Sequence 144, App
10	82.1	109	15 US-10-316-194-144	Sequence 35, App
11	79.5	109	15 US-10-316-194-35	Sequence 52, App
12	73.5	109	15 US-10-316-194-43	Sequence 43, Appl
13	52	1026	10 US-09-947-063-4	Sequence 4, Appl
14	52	1026	10 US-09-947-063-11	Sequence 11, Appl
15	41.9	49	9 US-09-728-912-7	Sequence 7, Appl

Query Match ID	Score	Length	DB ID	Description
1	100.0	23	9 US-09-991-548-11	Sequence 11, Appl
2	100.0	16	US-10-231-494-30	Sequence 30, Appl

**RESULT 2**

US-10-231-494-30  
 Sequence 30 Application US/10231494  
 Publication No. US20040023334A1  
 GENERAL INFORMATION:  
 APPLICANT: PRIOR, Christopher P.  
 TITLE OF INVENTION: Modified Transferrin Fusion Proteins  
 FILE REFERENCE: 547110-5001-US  
 CURRENT APPLICATION NUMBER: US/10/231,494  
 CURRENT FILING DATE: 2002-08-30  
 PRIOR APPLICATION NUMBER: US 60/315,745  
 PRIOR FILING DATE: 2001-08-30  
 PRIOR APPLICATION NUMBER: US 60/334,059  
 PRIOR FILING DATE: 2001-11-30  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 30  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic  
 OTHER INFORMATION: Peptide  
 US-10-231-494-30

Query Match 100.0%; Score 117; DB 16; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVETLEGTECVLSNLGRTRY 23  
 Db 1 QRVETLEGTECVLSNLGRTRY 23

**RESULT 3**

US-10-364-276-12  
 Sequence 12 Application US/10364276  
 Publication No. US200321544A1  
 GENERAL INFORMATION:  
 APPLICANT: Elliott, Steven G.  
 TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor  
 FILE REFERENCE: 06843-0030-04000  
 CURRENT APPLICATION NUMBER: US/10/364,276  
 CURRENT FILING DATE: 2003-06-17  
 PRIOR APPLICATION NUMBER: 09/092,671  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 08/280,864  
 PRIOR FILING DATE: 1994-07-26  
 PRIOR APPLICATION NUMBER: 09/640,090  
 PRIOR FILING DATE: 2000-08-17  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 12  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 OTHER INFORMATION: Peptide  
 US-10-364-276-12

Query Match 100.0%; Score 117; DB 15; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVETLEGTECVLSNLGRTRY 23  
 Db 1 QRVETLEGTECVLSNLGRTRY 23

**RESULT 4**

US-10-287-971-48

/ Sequence 48, Application US/10287971  
 / Publication No. US20040067882A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Alisbrook, et al.  
 / TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 / FILE REFERENCE: 21402-480A  
 / CURRENT APPLICATION NUMBER: US/10/287,971  
 / CURRENT FILING DATE: 2002-11-05  
 / PRIOR APPLICATION NUMBER: 09/997,425  
 / PRIOR FILING DATE: 2001-11-29  
 / PRIOR APPLICATION NUMBER: 10/035,568  
 / PRIOR FILING DATE: 2001-10-22  
 / PRIOR APPLICATION NUMBER: 60/338,626  
 / PRIOR FILING DATE: 2001-11-05  
 / PRIOR APPLICATION NUMBER: 60/401,479  
 / PRIOR FILING DATE: 2002-08-06  
 / PRIOR APPLICATION NUMBER: 60/333,072  
 / PRIOR FILING DATE: 2001-11-06  
 / PRIOR APPLICATION NUMBER: 60/348,283  
 / PRIOR FILING DATE: 2001-11-09  
 / PRIOR APPLICATION NUMBER: 60/393,262  
 / PRIOR FILING DATE: 2002-07-02  
 / PRIOR APPLICATION NUMBER: 60/406,181  
 / PRIOR FILING DATE: 2000-08-26  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 48  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / NUMBER OF SEQ ID NOS: 397  
 / SOFTWARE: Curaseqlist version 0.1  
 / SEQ ID NO: 50  
 / LENGTH: 455  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens

OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/016,159  
 FILING DATE: 30-JAN-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/876,227  
 FILING DATE: 16-JUN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/734,097  
 FILING DATE: 21-OCT-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/460,525  
 FILING DATE: 02-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billinger, Mark S.  
 REGISTRATION NUMBER: 34,812  
 REFERENCE/DOCKET NUMBER: 07004/002003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612/335-5070  
 TELEFAX: 612/288-9636  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 508 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-016-159-5

Query Match Score 117; DB 12; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 6  
 US-10-287-971-52  
 Sequence 52, Application US/10287971  
 Publication No. US2004006782A1  
 GENERAL INFORMATION:  
 APPLICANT: Alisbrook, et al  
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 FILE REFERENCE: 21402-480A  
 CURRENT FILING DATE: 2002-11-05  
 PRIOR APPLICATION NUMBER: 09/997,425  
 PRIOR FILING DATE: 2001-11-29  
 PRIOR APPLICATION NUMBER: 10/035,568  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: 60/338,626  
 PRIOR FILING DATE: 2001-11-05  
 PRIOR APPLICATION NUMBER: 60/401,479  
 PRIOR FILING DATE: 2002-08-06  
 PRIOR APPLICATION NUMBER: 60/333,072  
 PRIOR FILING DATE: 2001-11-06  
 PRIOR APPLICATION NUMBER: 60/348,283  
 PRIOR FILING DATE: 2001-11-09  
 PRIOR APPLICATION NUMBER: 60/393,262  
 PRIOR FILING DATE: 2002-07-02  
 PRIOR APPLICATION NUMBER: 60/406,181  
 PRIOR FILING DATE: 2002-08-26  
 NUMBER OF SEQ ID NOS: 397  
 SOFTWARE: CuraSeqList version 0.1  
 SEQ ID NO: 52  
 LENGTH: 458  
 TYPE: PRY  
 ORGANISM: Homo sapiens

US-10-287-971-52

Query Match Score 117; DB 12; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
 Matches 23; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 7  
 US-09-016-159-5  
 Sequence 5, Application US/09016159  
 Patent No. US20031806A1  
 GENERAL INFORMATION:  
 APPLICANT: Lee, Jong Y.  
 TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
 TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fish & Richardson P.C., P.A.  
 STREET: 60 South Sixth Street, Suite 3300  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM compatible

Query Match Score 113; DB 12; Length 508;  
 Query Match Score 117; DB 12; Length 508;

Best Local Matches	Local Similarity	Prod. No.	2.e-09;	Indels	Gaps	0;	Matches	20;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	
22;	Conservative						Qy	1	QRVBILLEGRTCEVLSNLRGRTRY	23							
Db	194	QKVILLNGRTCEVLSNLRGRTRY	216				Db	46	QRVBILNGRTCEVLSNLRGRTRY	68							
RESULT 9 US-10-316-194-142																	
; Sequence 142, Application US/10316194																	
; Publication No. US20030215914A1																	
; GENERAL INFORMATION:																	
; APPLICANT: Houtzager, Erwin																	
; APPLICANT: Vijn, Irma M.C.																	
; APPLICANT: Sijmons, Peter C.																	
; TITLE OF INVENTION: A structure for presenting desired peptide sequences																	
; FILE REFERENCE: 2183-5610US																	
; CURRENT APPLICATION NUMBER: US/10/316,194																	
; CURRENT FILING DATE: 2002-12-10																	
; PRIOR APPLICATION NUMBER: US 10/016,516																	
; PRIOR FILING DATE: 2001-12-10																	
; NUMBER OF SEQ ID NOS: 173																	
; SOFTWARE: PatentIn Ver. 2.1																	
; SEQ ID NO 35																	
; LENGTH: 109																	
; TYPE: PRT																	
; ORGANISM: Artificial Sequence																	
; FEATURE:																	
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid																	
; FEATURE:																	
; OTHER INFORMATION: Sequence of IMab600																	
; FEATURE:																	
; OTHER INFORMATION: Sequence of imab600																	
; NAME/KEY: SITE																	
; LOCATION: (1)..(109)																	
; US-10-316-194-35																	
Query Match 88.0%; Score 103; DB 15; Length 109;																	
Best Local Similarity 91.3%; Pred. No. 1.8e-08;																	
Matches 21; Conservative 0; Mismatches 2;																	
Indels 0; Gaps 0;																	
Qy 1 QRVBILLEGRTCEVLSNLRGRTRY 23																	
Db 46 QRVBILNGRTCEVLSNLRGRTRY 68																	
RESULT 10 US-10-316-194-144																	
; Sequence 144, Application US/10316194																	
; Publication No. US20030215914A1																	
; GENERAL INFORMATION:																	
; APPLICANT: Houtzager, Erwin																	
; APPLICANT: Vijn, Irma M.C.																	
; APPLICANT: Sijmons, Peter C.																	
; TITLE OF INVENTION: A structure for presenting desired peptide sequences																	
; FILE REFERENCE: 2183-5610US																	
; CURRENT APPLICATION NUMBER: US/10/316,194																	
; CURRENT FILING DATE: 2002-12-10																	
; PRIOR APPLICATION NUMBER: US 10/016,516																	
; PRIOR FILING DATE: 2001-12-10																	
; NUMBER OF SEQ ID NOS: 173																	
; SOFTWARE: PatentIn Ver. 2.1																	
; SEQ ID NO 43																	
; LENGTH: 109																	
; TYPE: PRT																	
; ORGANISM: Artificial Sequence																	
; FEATURE:																	
; OTHER INFORMATION: Description of Artificial Sequence: IMab100																	
; FEATURE:																	
; OTHER INFORMATION: Sequence of imab100																	
; NAME/KEY: SITE																	
; LOCATION: (1)..(109)																	
; US-10-316-194-43																	
Query Match 82.1%; Score 96; DB 15; Length 109;																	
Best Local Similarity 87.0%; Pred. No. 2.3e-07;																	
Qy 1 QRVBILNGRTCEVLSNLRGRTRY 68																	
Db 46 QRVBILNGRTCEVLSNLRGRTRY 68																	
RESULT 11 US-10-316-194-35																	
; Sequence 35, Application US/10316194																	
; Publication No. US20030215914A1																	
; GENERAL INFORMATION:																	
; APPLICANT: Houtzager, Erwin																	
; APPLICANT: Vijn, Irma M.C.																	
; APPLICANT: Sijmons, Peter C.																	
; TITLE OF INVENTION: A structure for presenting desired peptide sequences																	
; FILE REFERENCE: 2183-5610US																	
; CURRENT APPLICATION NUMBER: US/10/316,194																	
; CURRENT FILING DATE: 2002-12-10																	
; PRIOR APPLICATION NUMBER: US 10/016,516																	
; PRIOR FILING DATE: 2001-12-10																	
; NUMBER OF SEQ ID NOS: 173																	
; SOFTWARE: PatentIn Ver. 2.1																	
; SEQ ID NO 35																	
; LENGTH: 109																	
; TYPE: PRT																	
; ORGANISM: Artificial Sequence																	
; FEATURE:																	
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid																	
; FEATURE:																	
; OTHER INFORMATION: Sequence of imab600																	
; NAME/KEY: SITE																	
; LOCATION: (1)..(109)																	
; US-10-316-194-43																	
Query Match 73.5%; Score 86; DB 15; Length 109;																	
Best Local Similarity 87.0%; Pred. No. 2.3e-07;																	
Qy 1 QRVBILNGRTCEVLSNLRGRTRY 68																	
Db 46 QRVBILNGRTCEVLSNLRGRTRY 68																	

RESULT 13  
 US-09-947-063-4  
 Query 1 ORVEILEGRTTECVLSNLGRTRY 23  
 Db 46 ORVEILNLNGTSEVLSNLGRTRY 68

Best Local Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Patent No. US20010036643A1  
 GENERAL INFORMATION:  
 APPLICANT: Holloway, James L.  
 TITLE OF INVENTION: Tumor Necrosis Factor-Stimulated Gene  
 TITLE OF INVENTION: and Protein  
 FILE REFERENCE: 99-94US  
 CURRENT APPLICATION NUMBER: US/09/728,912  
 CURRENT FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: 60-169,252  
 PRIOR FILING DATE: 1999-12-06  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 7  
 LENGTH: 49  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-728-912-7

Query Match 41.9%; Score 49; DB 9; Length 49;  
 Best Local Similarity 50.0%; Pred. No. 2.4;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VELIERSRTTECVLSNLGRTR 22  
 Db 7 VELLDDGYTHVLARFHGRSR 26

Search completed: May 6, 2004, 12:48:22  
 Job time : 43 secs

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RESULT 14  
 US-09-947-063-11  
 Query 7 EGRTBCVLSNLGR 20  
 Db 292 EGFYECTASNLGR 305

Best Local Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Patent No. US20010036643A1  
 GENERAL INFORMATION:  
 APPLICANT: Padigaru, et al.  
 TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
 CURRENT APPLICATION NUMBER: US/09/947,063  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: 60-229,990  
 PRIOR FILING DATE: 2000-09-05  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 1026  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-947-063-4

Query Match 44.4%; Score 52; DB 10; Length 1026;  
 Best Local Similarity 71.4%; Pred. No. 27; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15  
 US-09-728-912-7  
 Query 7 EGRTBCVLSNLGR 20  
 Db 292 EGFYECTASNLGR 305

Best Local Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Patent No. US20010036643A1  
 GENERAL INFORMATION:  
 APPLICANT: Padigaru, et al.  
 TITLE OF INVENTION: No. US20030059775A1el Proteins and Nucleic Acids Encoding Same  
 CURRENT APPLICATION NUMBER: US/09/947,063  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: 60-229,990  
 PRIOR FILING DATE: 2000-09-05  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 11  
 LENGTH: 1026  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-947-063-11

Query Match 44.4%; Score 52; DB 10; Length 1026;  
 Best Local Similarity 71.4%; Pred. No. 27; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15  
 US-09-728-912-7  
 Sequence 7 Application US/0928912

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